

| Result No. | Score | Query | | | DB | ID | Description |
|------------|-------|-------|--------|---|-------------|--------|--------------|
| | | Match | Length | | | | |
| 1 | 811 | 99.9 | 193 | 1 | IL18_HUMAN | Q14116 | homo sapien |
| 2 | 659 | 81.2 | 193 | 1 | IL18_HORSE | Q9xaq7 | equus caball |
| 3 | 654 | 80.5 | 193 | 1 | IL18_BOVIN | Q9cu73 | bos taurus |
| 4 | 637 | 78.4 | 192 | 1 | IL18_PIG | Q19073 | bos scrofa |
| 5 | 613 | 75.5 | 193 | 1 | IL18_CANFA | Q9xsr0 | canis famil |
| 6 | 515 | 63.4 | 192 | 1 | IL18_MOUSE | P70380 | mus musculus |
| 7 | 514.5 | 63.4 | 194 | 1 | IL18_RAT | P97636 | rattus norv |
| 8 | 178.5 | 22.0 | 196 | 1 | IL18_CHICK | Q8cfq8 | gallus gall |
| 9 | 88 | 10.8 | 4705 | 1 | FAT2_DROME | Q9w71 | drosophila |
| 10 | 81.5 | 10.0 | 270 | 1 | IL1A_PIG | P18430 | sus scrofa |
| 11 | 81 | 10.0 | 267 | 1 | IL1A_RABIT | P84822 | oryctolagus |
| 12 | 80 | 9.9 | 1449 | 1 | DPO3_CLOPE | Q8xjr3 | clostridium |
| 13 | 77.5 | 9.5 | 674 | 1 | MUTL_CLOPE | Q8x186 | clostridium |
| 14 | 76.5 | 9.4 | 270 | 1 | IL1A_HORSE | Q28385 | equus caball |
| 15 | 75.5 | 9.3 | 192 | 1 | OASB_MOUSE | Q60856 | mus musculus |
| 16 | 75.5 | 9.3 | 1036 | 1 | X414_MYCGE | P47653 | mycoplasma |
| 17 | 75.5 | 9.3 | 1863 | 1 | C03_MOUSE | P01027 | mus musculus |
| 18 | 74.5 | 9.2 | 1228 | 1 | ECM_HUMAN | Q13201 | homo sapien |
| 19 | 74 | 9.1 | 467 | 1 | M3K8_MOUSE | Q07174 | mus musculus |
| 20 | 74 | 9.1 | 467 | 1 | M3K8_RAT | Q63562 | rattus norv |
| 21 | 74 | 9.1 | 1772 | 1 | MSP1_PLAYO | P13828 | plasmodium |
| 22 | 73 | 9.0 | 270 | 1 | IL1A_FELCA | Q48613 | felis silve |
| 23 | 73 | 9.0 | 418 | 1 | SVS_UREPA | Q9pr38 | ureaplasma |
| 24 | 73 | 9.0 | 426 | 1 | YXCX_ASTILO | P58151 | astasia lon |
| 25 | 72.5 | 8.9 | 313 | 1 | C0L4_ARATH | Q9m9b3 | arabidopsis |
| 26 | 72.5 | 8.9 | 412 | 1 | UVSE_CLOPE | Q8xip3 | clostridium |
| 27 | 71.5 | 8.8 | 268 | 1 | IL1A_BOVIN | P08831 | bos taurus |
| 28 | 71.5 | 8.8 | 467 | 1 | M3K8_HUMAN | P41279 | homo sapien |
| 29 | 71.5 | 8.8 | 527 | 1 | RAG2_HUMAN | P55895 | homo sapien |
| 30 | 71 | 8.7 | 700 | 1 | NONA_DROME | Q04047 | drosophila |
| 31 | 70.5 | 8.7 | 245 | 1 | KDSB_FUSUN | Q8xfaf | fusobacteri |
| 32 | 70.5 | 8.7 | 268 | 1 | IL1A_CAPHI | P79161 | capra hircu |
| 33 | 70.5 | 8.7 | 644 | 1 | YGM4_YEAST | P53129 | saccharomyc |

RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]

RN SEQUENCE OF 2-193 FROM N.A.

RC TISSUE=peripheral blood;

RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS

CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I

CC CELLS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the IL-1 family.

CC -----
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 CC -----

EMBL; D49950; BAA08706.1; -

EMBL; AF077611; AAC27787.1; -

EMBL; AY044641; AAK95950.1; -

EMBL; BC007007; AAH07007.1; -

EMBL; BC007461; AAH07461.1; -

EMBL; U90434; AAB50010.1; -

Genew; HGNC:15986; IL18.

MIM; 600953; -

DR GO; GO:0005576; C:cytoplasmic; TAS.

DR GO; GO:0016506; F:apoptosis activator activity; ISS.

DR GO; GO:004871; F:signal transducer activity; TAS.

DR GO; GO:0001525; P:angiogenesis; IDA.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0042033; P:chemokine biosynthesis; TAS.

DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . . ; TAS.

DR GO; GO:0006955; P:immune response; TAS.

DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . . ; ISS.

DR GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.

DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.

DR GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.

DR GO; GO:0042104; P:positive regulation of activated T-cell pro. . . ; IDA.

DR GO; GO:0030155; P:regulation of cell adhesion; IDA.

DR GO; GO:0030431; P:sleep; ISS.

DR GO; GO:0042092; P:T-helper 2 type immune response; TAS.

DR InterPro; IPR000975; Interleukin_1.

DR SMART; SM00125; IL1; 1.

KW Cytokine.

FT CHAIN 1 36 BY SIMILARITY.

FT PROPEP 37 193 INTERLEUKIN-18.

FT CONFLICT 66 66 F -> L (IN REF. 2).

FT CONFLICT 86 86 S -> R (IN REF. 2).

FT CONFLICT 191 191 N -> S (IN REF. 2).

FT SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 1; Length 193;

Best Local Similarity 99.4%; Pred. No. 7.9e-69;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDAPRTIFIISMYKDSQPRGM 60

DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISKLSCENKIISFKENPPDNKDTSKDIIFQRSVPGHDKNQPFESSY 120

DB 97 AVTISVKCEKISKLSCENKIISFKENPPDNKDTSKDIIFQRSVPGHDKNQPFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 157

DB 157 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 193

RESULT 2

IL18_HORSE

ID IL18_HORSE STANDARD; PRT; 193 AA.

AC Q9XSG7;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)

DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).

GN IL18 OR IGIP.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;

RN [1]_TaxID=9796;

RP SEQUENCE FROM N.A.

RA Nicolson L., Fenna-Goncalves M.N., Keanie J.L., Logan N.A.,

RA Argyle D.J., Onions D.E.;

RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS

CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I

CC CELLS (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the IL-1 family.

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EMBL; Y11131; CAAY2013.1; -

KW Cytokine.

FT PROPEP 1 36 BY SIMILARITY.

FT CHAIN 37 193 INTERLEUKIN-18.

FT SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAC CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;

Best Local Similarity 77.7%; Pred. No. 1.2e-54;

Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDAPRTIFIISMYKDSQPRGM 60

DB 37 YFGRLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCDNDAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISKLSCENKIISFKENPPDNKDTSKDIIFQRSVPGHDKNQPFESSY 120

DB 97 AVTISVKCEKISKLSCENKIISFKENPPDNKDTSKDIIFQRSVPGHDKNQPFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 157

DB 157 KGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 193

RESULT 3

IL18_BOVIN

ID IL18_BOVIN STANDARD; PRT; 193 AA.

AC Q9TU73;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)

DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).

GN IL18.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RL 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF124789; AAF08686.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 3.6e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESLVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFIIISWKDSQPRGM 60
Db 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMDPSDCSDNAPQTVIIYWKDSLTRL 96

Qy 61 AVTISVCKEKISXLSCKENKIISPKENPPDNIKDTKSDIIFQSVPGHDKMOPFESSY 120
Db 97 AVTISVQCKKMTLSCKNKITLSPKEMSPDPNIDEGNDIIFQSVPGHDDKIQFESSLY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 KGYFLACKKENDLFLKILKQDDNRDKSVWFTVQNK 193

RESULT 4
IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.

```

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RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dosois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RT Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:358-365(2000).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC
DR EMBL; U68701; AAC18415.1; -
DR EMBL; Y11132; CAA72014.1; -
DR EMBL; AB010003; BAA24135.1; -
DR EMBL; AF191088; AAF71200.1; -
DR GO; GO:0005576; P:extracellular; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 1.4e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESLVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFIIISWKDSQPRGM 60
Db 36 YFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMDPSDCSDNAPQTVIIYWKDSLTRL 95

Qy 61 AVTISVCKEKISXLSCKENKIISPKENPPDNIKDTKSDIIFQSVPGHDKMOPFESSY 120
Db 96 AVTISVQCKKMTLSCKNKITLSPKEMSPDPNIDEGNDIIFQSVPGHDDKIQFESSLY 155

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 156 KGYFLACKKENDLFLKILKKEDEGDKSIMFTVQNK 192

RESULT 5
IL18_CANFA STANDARD; PRT; 193 AA.
AC Q9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309818; PubMed=10380699;

```

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RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;  
RT "Cloning, sequencing, and characterization of dog interleukin-18.";  
RL Immunogenetics 49:541-543 (1999).  
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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CC  
CC EMBL: Y11133; CAAT2015.1; -  
CC GO: GO:0005576; C:extracellular; TAS.  
CC GO: GO:0016506; F:apoptosis activator activity; IEP.  
CC GO: GO:0005125; F:cytokine activity; TAS.  
CC GO: GO:0042033; P:chemokine biosynthesis; ISS.  
CC GO: GO:0008625; P:induction of apoptosis via death domain rec. . .; IEP.  
CC GO: GO:0042095; P:interferon-gamma biosynthesis; IDA.  
CC GO: GO:0042104; P:positive regulation of activated T-cell pro. . .; ISS.  
CC Cytokine.  
KW PROPEP 1 36 BY SIMILARITY  
FT CHAIN 37 193 INTERLEUKIN-18  
FT SEQUENCE 193 AA; 22037 MW; 0D973E86F461F25 CRC64;  
Query Match 75.5%; Score 613; DB 1; Length 193;  
Best Local Similarity 73.7%; Pred. No. 2.4e-50;  
Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGM 60  
Db YFGKLEPKLSIIRNLNDQVLFVNEGNQPVFEDMPDSDCTDNAPHTIFIIYMYKDSLTRLG 96  
QY 61 AVTISVKCEKISXLSCKNIISFKENPPDNTKDTKSDIIFQSVPGHDKNQMFESSY 120  
Db AVTISVKYKTMSTLSCKNKTISFQKSPDPSINDEGNDIIFQSVPGHDKNQMFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 156  
Db KGHFLACKENDLFLKILKDKOENGKSVNFTVQNK 192  
RESULT 6  
IL18 MOUSE  
ID IL18 MOUSE STANDARD; PRT; 192 AA.  
AC P70350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
GN IL18 OR IGIF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=96061009; PubMed=7477296;  
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,  
RA Tanimoto T., Torioke K., Okura T., Nukada Y., Hattori K.,  
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;  
RT "Cloning of a new cytokine that induces IFN-gamma production by T  
RT cells.";  
RL Nature 378:88-91 (1995).  
RN [2]  
RP SEQUENCE OF 1-191 FROM N.A.
```

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RC STRAIN=NOD; TISSUE=Pancreas;  
RX MEDLINE=97174346; PubMed=9022080;  
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;  
RT "Active stage of autoimmune diabetes is associated with the  
RT expression of a novel cytokine, IGIF, which is located near Idd2.";  
RL J. Clin. Invest. 99:469-474 (1997).  
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
CC CELLS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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CC  
CC EMBL: D49949; BAA08705.1; -  
CC PIR: S60226; ABA49753.1; -  
CC MGD: MGI:107936; I118.  
CC GO: GO:0005576; C:extracellular; ISS.  
CC GO: GO:0016506; F:apoptosis activator activity; TAS.  
CC GO: GO:0001525; F:angiogenesis; ISS.  
CC GO: GO:0042033; P:chemokine biosynthesis; ISS.  
CC GO: GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; ISS.  
CC GO: GO:0008625; P:induction of apoptosis via death domain rec. . .; TAS.  
CC GO: GO:0042095; P:interferon-gamma biosynthesis; IMP.  
CC GO: GO:0042231; P:interleukin-13 biosynthesis; TAS.  
CC GO: GO:0042094; P:interleukin-2 biosynthesis; ISS.  
CC GO: GO:0042104; P:positive regulation of activated T-cell pro. . .; ISS.  
CC GO: GO:0030155; P:regulation of cell adhesion; ISS.  
CC GO: GO:0030431; P:sleep; ISS.  
CC InterPro; IPR000975; Interleukin_1.  
CC Pfam; PF00340; IL1; 1.  
CC SMART; SM00125; IL1; 1.  
KW Cytokine.  
FT PROPEP 1 35  
FT CHAIN 36 192 INTERLEUKIN-18.  
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).  
FT SEQUENCE 192 AA; 22135 MW; 8FD938473874D63 CRC64;  
Query Match 63.4%; Score 515; DB 1; Length 192;  
Best Local Similarity 64.9%; Pred. No. 3.4e-41;  
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;  
QY 2 FGLKESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGWA 61  
Db FGLHCTTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIYMYKDSVGRGUA 95  
QY 62 VTISVKCEKISXLSCKNIISFKENPPDNTKDTKSDIIFQSVPGHDKNQMFESSY 121  
Db VTLVKDSKMSLTSLCKNLTISFEENDPPENIDDIQSDLIFFQKRVFGH-NKMEFESSLYE 154  
QY 122 GYFLACEKERDLFKLILKKEDELGRSINFTVQNE 155  
Db GHFLACQEDDAPKILKDKOENGKSVNFTVQNK 188  
RESULT 7  
IL18 RAT  
ID IL18 RAT STANDARD; PRT; 194 AA.  
AC P97636; O88749; P97637;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
GN IL18 OR IGIF.  
OS Rattus norvegicus (Rat).
```

```

Qy 121 EGYPLACEKRDLPFKLILKKEDLGDRSMTFTVN 150
    |||:||||| |||:|||||:|||||:|||
Db 156 EGFLACQCKDDAFKLVLKRDKDENGSKSYMFTLTN 190

RESULT 8
ID IL18 CHICK STANDARD; PRT; 196 AA.
AC QSOQF08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE DE Interleukin-18 precursor (IL-18).
GN IL18.
OC Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phas-
OX Gallus.
CN NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rothwell L., Buerstedde J.M., Kaiser P.;
RT "Cloning and Characterisation of chicken interleukin-18
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ dat-
CC -|- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIV-
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN
CC CELLS (By similarity).
CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -|- SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced
CC between the Swiss Institute of Bioinformatics &
CC the European Bioinformatics Institute. There are no
CC use by non-profit institutions as long as it is
CC modified and this statement is not removed. Unpub-
CC entities requires a license agreement (See http://
CC or send an email to license@ebi.ac.uk).

EMBL; AJ276025; CACB1652.1; -.
CYCOTKINE.
KW PROPEP
FT CHAIN
SQ SEQUENCE 196 AA; 22787 MW; 4947DCECCB32414 (
Query Match 22.0%; Score 178.5; DB 1;
Best Local Similarity 34.3%; Pred. NO. 9e-10;
Matches 60; Conservative 26; Mismatches 68;

Qy 1 YFGKLESL-----SVIRNLNDVLFIDOG-NRPLF
Db 20 YFESECDACFKDKTKTRFRNVNSQLLVPRDLNVAAFI
Qy 52 YKDSQPRG-MAVTVISVKCEKIKSLXSCNK-----IISFKKI
Db 79 YKTTAPSARMVPVAFSVQVEDKSYWCCEKEHGKMWVRFR
Qy 106 VPGHDNK-MQFESSSSYEGVFPLACEKERDLFKLIK--H
Db 138 FTSCSSKAFFKFEYSLEQGFMFLAFEEEDSLRKLIILKLPRI

RESULT 9
ID FAT2_DROME
AC ID FAT2 DROME STANDARD; PRT; 4705 AA.
IC Q9VMW71; Q95S51;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative fat-like cadherin-related tumor suppress-
DE precursor.
GN FAT2 OR CG7749.
OS Drosophila melanogaster (Fruit fly).
```

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA DuYbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Glodek A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Hooten C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP REVISIONS.
 RC STRAIN=Berkley;
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [3]
 RP SEQUENCE OF 3837-4705 FROM N.A.
 RC STRAIN=Berkley; TISSUE=Ovary;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 34 cadherin domains.
 CC -1- SIMILARITY: Contains 5 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 laminin G-like domain.

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EMBL; AE003515; AAP49078.2; -
 EMBL; AY060955; AAL28503.1; ALT_INIT.
 EMBL; AY118666; AAM50035.1; ALT_INIT.
 HSSP; P51116; INCI.
 FlyBase; FBgn0036930; fat2.
 GO; GO:0005887; C:integral to plasma membrane; ISS.
 GO; GO:0008014; F:calcium-dependent cell adhesion molecule ac. . . ; ISS.
 GO; GO:0016339; P:calcium-dependent cell-cell adhesion; ISS.
 InterPro; IPR000152; Asx_hydroxyl.
 InterPro; IPR001881; EGF Ca.
 InterPro; IPR006209; EGF-like.
 InterPro; IPR006210; IEGF.
 InterPro; IPR001791; Laminin G.
 Pfam; PF000028; cadherin; 31.
 Pfam; PF00008; EGF; 5.
 Pfam; PF00054; laminin G; 1.
 PRINTS; PR00205; CADHERIN.
 SMART; SM00112; CA; 34.
 SMART; SM00181; EGF; 6.
 SMART; SM00282; LamG; 1.
 PROSITE; PS00010; ASX HYDROXYL; 1.
 PROSITE; PS00232; CADHERIN_1; 18.
 PROSITE; PS0268; CADHERIN_2; 34.
 PROSITE; PS00022; EGF_1; 5.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS01187; EGF CA; 1.
 PROSITE; PS00025; LAM G DOMAIN; 1.
 KW Hypothetical protein; Cell adhesion; Signal; Glycoprotein;
 KW Transmembrane; Calcium; Calcium-binding; Repeat; EGF-like domain.
 FT SIGNAL 1 35 POTENTIAL
 FT CHAIN 36 4705 PUTATIVE FAT-LIKE CADHERIN-RELATED TUMOR
 FT SUPPRESSOR HOMOLOG.
 FT DOMAIN 1648 1668 POTENTIAL.
 FT DOMAIN 1669 4705 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 60 180 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 181 288 CADHERIN 1.
 FT DOMAIN 285 397 CADHERIN 2.
 FT DOMAIN 398 504 CADHERIN 3.
 FT DOMAIN 505 610 CADHERIN 4.
 FT DOMAIN 611 713 CADHERIN 5.
 FT DOMAIN 770 874 CADHERIN 6.
 FT DOMAIN 875 977 CADHERIN 7.
 FT DOMAIN 978 1085 CADHERIN 8.
 FT DOMAIN 1086 1195 CADHERIN 9.
 FT DOMAIN 1191 1296 CADHERIN 10.
 FT DOMAIN 1297 1402 CADHERIN 11.
 FT DOMAIN 1403 1503 CADHERIN 12.
 FT DOMAIN 1504 1609 CADHERIN 13.
 FT DOMAIN 1610 1714 CADHERIN 14.
 FT DOMAIN 1715 1812 CADHERIN 15.
 FT DOMAIN 1813 1929 CADHERIN 16.
 FT DOMAIN 1930 2030 CADHERIN 17.
 FT DOMAIN 2031 2137 CADHERIN 18.
 FT DOMAIN 2138 2238 CADHERIN 19.
 FT DOMAIN 2239 2338 CADHERIN 20.
 FT DOMAIN 2339 2465 CADHERIN 21.
 FT DOMAIN 2466 2567 CADHERIN 22.
 FT DOMAIN 2568 2670 CADHERIN 23.
 FT DOMAIN 2671 2779 CADHERIN 24.
 FT DOMAIN 2780 2876 CADHERIN 25.
 FT DOMAIN 2877 2983 CADHERIN 26.
 FT DOMAIN 2984 3088 CADHERIN 27.
 FT DOMAIN 2985 3088 CADHERIN 28.

FT DOMAIN 3084 3185 CADHERIN 29.
 FT DOMAIN 3186 3289 CADHERIN 30.
 FT DOMAIN 3290 3394 CADHERIN 31.
 FT DOMAIN 3395 3499 CADHERIN 32.
 FT DOMAIN 3500 3604 CADHERIN 33.
 FT DOMAIN 3605 3712 CADHERIN 34.
 FT DOMAIN 3819 3879 EGF-LIKE 1.
 FT DOMAIN 3881 3919 EGF-LIKE 2.
 FT DOMAIN 3937 4121 LAMININ G-LIKE.
 FT DOMAIN 4129 4166 EGF-LIKE 3.
 FT DOMAIN 4168 4205 EGF-LIKE 4.
 FT DOMAIN 4243 4279 EGF-LIKE 5.
 FT DISULFID 3823 3835 POTENTIAL.
 FT DISULFID 3830 3867 POTENTIAL.
 FT DISULFID 3869 3878 POTENTIAL.
 FT DISULFID 3885 3896 POTENTIAL.
 FT DISULFID 3890 3907 POTENTIAL.
 FT DISULFID 3909 3918 POTENTIAL.
 FT DISULFID 4133 4144 POTENTIAL.
 FT DISULFID 4138 4154 POTENTIAL.
 FT DISULFID 4156 4165 POTENTIAL.
 FT DISULFID 4172 4183 POTENTIAL.
 FT DISULFID 4177 4193 POTENTIAL.
 FT DISULFID 4195 4204 POTENTIAL.
 FT DISULFID 4247 4258 POTENTIAL.
 FT DISULFID 4252 4267 POTENTIAL.
 FT DISULFID 4269 4278 POTENTIAL.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 3962 3962 G -> E (IN REF. 3; AAL28503).
 SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match 10.8%; Score 88; DB 1; Length 4705;
 Best Local Similarity 23.6%; Pred. No. 11;
 Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY " 32 DWTSDCDNAPRTIFLIISMY-----KDSQPRGMATISVKCEKISXLSCEKNIISF--KE 85
 DB 2124 DISVLVDVNDNCP--LFFVNNPYATVSIIDPKG---TIIMQVKAIDLDSAEENGVEVYELK 2178
 QY 86 MNPPDNIKDTSIIFFORSVPGHDKMQPFESSYEGYFLACEKERDL----- 133
 DB 2179 NGELFKLDRKSGELSIKHQVGEHNRNVELTVAAVDGAIPTCCSSAPLOVKVIDRSMVPV 2238
 QY 134 ---FKLIKKED-----ELGDRSIMFTVQNE 156
 DB 2239 EKQFTVSVKEDVEMYALSVSIAESPLG-RSLIVTISSE 2278

RESULT 10

IL1A_PIG STANDARD; PRT; 270 AA.
 AC P18430;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-1 alpha precursor (IL-1 alpha).
 GN IL1A.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

Query Match 10.0%; Score 81.5; DB 1; Length 270;
 Best Local Similarity 22.7%; Pred. No. 1.5;
 Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

QY 8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD-----SCDRDNAPRTI-FIISMYKDSQPRGMAY 62
 DB 123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAAVLNNLDEAVKFDMAAYTSDNDSQLPV 182
 QY 63 TISVKEKISXLSCE--KIISPKEM-NPPDNIKDTSIIFFORSVPGHDKMQPFESS 119
 DB 183 TLIRIS-ETRLFVSAQNEDEPVLKELPPTKTIKDETSLLFFWEK-----HGNMDFKSA 237
 QY 120 YEGYFLACEKER 131
 DB 238 HPKLFIAIATRQEK 249

RESULT 11
 IL1A_RABIT

RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=90332454; PubMed=2377484;
 RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
 Baker P.E.;
 RT "porcine IL-1 alpha cDNA nucleotide sequence.";
 RL Nucleic Acids Res. 18:4282-4282(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huether M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
 RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: Monomer.
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: Belongs to the IL-1 family.

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 or send an email to license@sib-sib.ch.

EMBL; X52731; CAA36945.1; -;
 EMBL; M86730; AAA73198.1; -;
 PIR; I46620; I46620.
 PIR; S10532; S10532.
 HSSP; P01583; LITA.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR Pfam; PF02394; IL1_propep; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN 1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 112
 FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 89 89 N -> I (IN REF. 2).
 FT CONFLICT 242 242 F -> L (IN REF. 2).
 FT CONFLICT 255 255 P -> R (IN REF. 2).
 SQ SEQUENCE 270 AA; 30788 MW; 5677BF2B0EF63839 CRC64;

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ID ILIA RABBIT STANDARD; PRT; 267 AA.
AC P04822;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297782; PubMed=2994016;
RA Furutani Y., Norake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Kakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
RT interleukin-1 precursor."
RL Nucleic Acids Res. 13:5869-5882(1985).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X02852; CAA26605.1; -.
CC HSP; P01583; IITA.
CC InterPro: IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 267 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 64 64 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 267 AA; 30375 MW; 6D20533FD1FA4822 CRC64;
Query Match 10.0%; Score 81; DB 1; Length 267;
Best Local Similarity 25.2%; Pred. No. 1.6;
Matches 32; Conservative 27; Mismatches 56; Indels 12; Gaps 5;
QY 12 IRLNDQVLFDQGNRPLFEDMTDSDCRDNPARTI-----FIISMYKDSQPRGMVITISV 66
DB 127 LRIKQEFNLNDALNSQLVSDQVLRAPLQNLGDAVKFMGVNTSDSILPVLRI 186
QY 67 KCKSIKSLSCEN--KIISPKEM-NPPDNINKDTKSDIIFQFORSVPGHDKNMQFSSSYEGY 123
DB 187 SQPLF-FVSAQNDEPVLKEMPETPRIITDSDSLFFWET---QGNKNYFKSAANPOL 242
QY 124 FLACEKE 130
DB 243 FIATKPE 249

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RESULT 12
DPO3_CLOPE STANDARD; PRT; 1449 AA.
AC Q8XJR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN POLC-OR CPE1691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC
CC SUBFAMILY.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF003191; BAB81397.1; -.
CC HAMAP; MF_00356; -; 1.
CC InterPro: IPR006054; DnaQ.
CC InterPro: IPR006055; Exonuclease.
CC InterPro: IPR004013; PHP_C.
CC InterPro: IPR003141; PHP_N.
CC InterPro: IPR006308; PolC_gram_pos.
CC Pfam; PF02811; PHP_C; 1.
CC Pfam; PF02811; PHP_N; 1.
CC SMART; SM00479; EXOIII; 1.
CC SMART; SM00481; POLIIIAC; 1.
CC TIGRFAM; TIGR00573; dnaq; 1.
CC TIGRFAM; TIGR01405; polC_Gram_pos; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Nuclease; Exonuclease; Complete proteome.
FT DOMAIN 435 598 EXONUCLEASE.
SQ SEQUENCE 1449 AA; 163627 MW; AE24E2CE7D372B85 CRC64;
Query Match 9.9%; Score 80; DB 1; Length 1449;
Best Local Similarity 27.2%; Pred. No. 15;
Matches 43; Conservative 21; Mismatches 52; Indels 42; Gaps 10;
QY 15 LNDQVLFDQGNRPLFEDMTDSDC---RDNAPRTFIISMYKDSQPRGMVITISVCKEKI 71
DB 1196 LNNQAQYFIKEGYTTL-----KDCIATRDD---IMVLYMYKDLPPK-TAFTIMEKVRG 1244
QY 72 SXLSCENKIISPKEMNPPD-NITKDTKSDIIFQFORSVPGHD-----NKMQFSS 118
DB 1245 KGLSEDEAL-NREKNVPDWYIESCKIKYMPK---GHAVAYVMVAIVYKYYPEA 1300
QY 119 SYEGYF-----LACEKERDLFKLILKKEDELGD 146

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Db      1301 YTTTFTVRADDFDADLICKGE-EAIKAKWEELNSIGN 1337
RESULT 13
MUTL_CLOPE
ID      MUTL_CLOPE      STANDARD;      PRT;      674 AA.
AC      Q8XL86;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      DNA mismatch repair protein mutL.
GN      MUTL OR CPE1156
OS      Clostridium perfringens.
OC      Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC      Clostridium.
OX      NCBI_TaxID=1502;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=13 / Type A;
RX      MEDLINE=21664373; PubMed=11792842;
RA      Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA      Shiba T., Ogawara N., Hattori M., Kuhara S., Hayashi H.;
RT      "Complete genome sequence of Clostridium perfringens, an anaerobic
RT      flesh-eater.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
CC      -!- FUNCTION: This protein is involved in the repair of mismatches in
CC      DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC      repair. May act as a "molecular matchmaker", a protein that
CC      promotes the formation of a stable complex between two or more
CC      DNA-binding proteins in an ATP-dependent manner without itself
CC      being part of a final effector complex (By similarity).
CC      -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEX FAMILY.
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CC      or send an email to license@isb-sib.ch).
DR      EMBL; AP003189; BAB80862.1; -.
DR      HAMAP; MF_00149; -.
DR      InterPro; IPR003594; ATPbind_ATPase.
DR      InterPro; IPR002099; DNA_mis_repair.
DR      Pfam; PF01119; DNA_mis_repair; 1.
DR      Pfam; PF03518; HATPase_c; 1.
DR      SMART; SM00387; HATPase_c; 1.
DR      TIGRFAMs; TIGR00585; mutL; 1.
DR      PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
KW      DNA repair; Complete proteome.
SQ      SEQUENCE 674 AA; 77205 MW; 2380566BB4500A3D CRC64;

Query Match      9.5%; Score 77.5; DB 1; Length 674;
Best Local Similarity 25.9%; Pred. No. 10;
Matches 30; Conservative 15; Mismatches 40; Indels 31; Gaps 5;

QY      17 DQVLFIDQGNRLFE-----DMTSDCR-----DNAPRTFIISMYKDSQPRGMA 61
Db      547 EDLYDE-NKEIFKAGFKISDFGNSIRIEEVPYFLDKLNPTLITSMINLNKMGVTG 605

QY      62 VTISVKCKISXLSCE-----NKISFKEM-----NPPDNKOTKSDIIEF 102
Db      606 ETVEKYNKIASMSCRAAVKANDVLSILEMENLIEDLAYINDPFPCHGRPTIIEF 661

RESULT 14
IL1A_HORSE
ID      IL1A_HORSE      STANDARD;      PRT;      270 AA.
AC      Q28385; O77743;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)

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DE      Interleukin-1 alpha precursor (IL-1 alpha).
GN      IL1A.
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96131982; PubMed=8578682;
RA      Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuoka R.,
RA      Tsujimoto H., Hasegawa A.;
RT      "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL      Vet. Immunol. Immunopathol. 48:221-231 (1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98285941; PubMed=9622738;
RA      Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT      "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
RT      and determination of their full-length cDNA sequences.";
RL      Am. J. Vet. Res. 59:704-711 (1998).
CC      -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC      THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC      MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC      IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC      IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC      THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC      (BY SIMILARITY).
CC      -!- SUBUNIT: Monomer (By similarity).
CC      -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC      AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC      -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC      PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC      OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC      SECRETORY PROTEINS.
CC      -!- SIMILARITY: Belongs to the IL-1 family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
DR      EMBL; D42146; BAA07717.1; -.
DR      EMBL; U92480; AAC39255.1; -.
DR      HSRP; P01583; IITA.
DR      InterPro; IPR003502; IL1_propep.
DR      InterPro; IPR000975; Interleukin_1.
DR      Pfam; PF00340; IL1; 1.
DR      Pfam; PF02394; IL1_propep; 1.
DR      SMART; SM00125; IL1; 1.
DR      PROSITE; PS00253; INTERLEUKIN_1; 1.
KW      Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT      PROPEP      1 112      BY SIMILARITY.
FT      CHAIN      113 270      INTERLEUKIN-1 ALPHA.
FT      CARBOHYD      141 141      N-LINKED (GLCNAC... ) (POTENTIAL).
FT      CONFLICT      110 110      R -> K (IN REF. 2).
FT      CONFLICT      150 150      G -> V (IN REF. 2).
SQ      SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;

Query Match      9.4%; Score 76.5; DB 1; Length 270;
Best Local Similarity 22.3%; Pred. No. 4.4;
Matches 29; Conservative 28; Mismatches 62; Indels 11; Gaps 4;

QY      7 SKLSVIRNLNDQVLFIDQGNRLPFEDMTSDCRDNAPRTI-----FIISMYKDSQPRGMA 61
Db      122 TKYNFMRIVNHQCTLNDALNQSVIRDTSGQYLATAALNNLNDVAVKFDGAVTSEDSQLP 181

QY      62 VTISV-KCEKISXLSCEKNIISFKEM-NPPDNKOTKSDIIEFFORSVPGHGNKQKFESS 119
Db      182 VTLRISKTRLFVSAQNEDEPVLLKEMPDPPTKINDETNLLFFWER----HGSKNYPKSA 237

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Search completed: December 12, 2003, 17:52:55
Job time : 17 secs

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RESULT 15
OASB_MOUSE STANDARD; PRT; 192 AA.
ID OASB_MOUSE STANDARD; PRT; 192 AA.
AC Q60856;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 2-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)
DE synthetase 1B) (2-5A synthetase 1B) (Fragment).
DN OAS1B OR OIAS2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=91232962; PubMed=1709495;
RT Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;
RA "The murine 2-5A synthetase locus: three distinct transcripts from two
RT linked genes."
RL Nucleic Acids Res. 19:1917-1924 (1991).
CC -1- FUNCTION: THE 2-5A SYSTEM (THE OASS, 2-5A, AND RNASE L) MAY PLAY A
CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
CC INTO PPP(A2'P5'A)N oligomers, which activate the latent RNASE L
CC that, when activated, cleaves single-stranded RNAs.
CC -1- INDUCTION: By interferons.
CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
CC
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CC
CC EMBL; X55982; CAA39455.1; -.
DR PIR; S15661; S15661.
DR MGD; MGI:97430; Oas1b.
DR GO; GO:0003800; F:antiviral response protein activity; IDA.
DR InterPro; IPR06117; 25A_SYNTH_2.
DR InterPro; IPR06116; 25A_synth_UB.
DR InterPro; IPR001201; PAP_25A_core.
DR PROSITE; PS00832; 25A_SYNTH_1; PARTIAL.
DR PROSITE; PS00833; 25A_SYNTH_2; PARTIAL.
DR PROSITE; PS0152; 25A_SYNTH_3; 1.
KW RNA-binding; Transferase; Nucleotidyltransferase;
KW Interferon induction.
FT NON_TER 1
FT NON_TER 192
FT FT 192
SQ SEQUENCE 192 AA; 21936 MW; 4E1C011BF9024F46 CRC64;

Query Match 9.3%; Score 75.5; DB 1; Length 192;
Rest Local Similarity 23.2%; Pred No.3.6;
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKD 54
Db 11 GRSDALVPLNNLTSFEDQLNQGVLLKIKQLCEVQHERRC----- 54
QY 55 SQRGRMAVTVSVKCEKSLXSCENKILSFKEKMPNPNKIDTKSDII----- 100
Db 55 -----GVKFEVHLSRPNRSALSFK-LSAPDLLKEVKEFDVLPAYDLLHLMLKK 103
QY 101 -----FFQR-----SVP-GHDNRNQVFESSYEGYFLACE--KERDLFKLI-----LKKEDELG 145

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:50:20 ; Search time 35 Seconds
(without alignments)
1157.550 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 798 | 98.3 | 193 | 4 Q96KJ8 | Q96KJ8 homo sapien |
| 2 | 792 | 97.5 | 193 | 6 Q9EG15 | Q9EG15 macaca mula |
| 3 | 654 | 80.5 | 178 | 6 Q9MZL8 | Q9MZL8 bos taurus |
| 4 | 648 | 79.8 | 193 | 6 Q9GLO9 | Q9GLO9 ovis aries |
| 5 | 634 | 78.1 | 192 | 6 Q95M33 | Q95M33 felis silve |
| 6 | 626 | 77.1 | 192 | 6 Q9N1P7 | Q9N1P7 eus scrofa |
| 7 | 441 | 54.3 | 196 | 11 Q91266 | Q91266 sigmodon hi |
| 8 | 313 | 38.5 | 84 | 6 Q9SLE7 | Q9SLE7 canis fami |
| 9 | 204 | 25.1 | 45 | 4 Q9NQ49 | Q9NQ49 homo sapien |
| 10 | 193 | 23.8 | 211 | 13 Q98SQ1 | Q98SQ1 anas platyr |
| 11 | 184.5 | 22.7 | 198 | 13 Q9AV26 | Q9AV26 melesgris |
| 12 | 182.5 | 22.5 | 198 | 13 Q918D2 | Q918D2 gallus gall |
| 13 | 86.5 | 10.7 | 376 | 11 Q8K4E7 | Q8K4E7 mus musculu |
| 14 | 86.5 | 10.7 | 376 | 11 Q8K4E6 | Q8K4E6 mus musculu |
| 15 | 85 | 10.5 | 252 | 11 Q8JZN4 | Q8JZN4 mus musculu |
| 16 | 85 | 10.5 | 381 | 3 Q43031 | Q43031 schizosacch |

| | | | | | |
|----|------|------|-------|-----------|--------------------|
| 17 | 84.5 | 10.4 | 376 | 11 Q8K4E8 | Q8K4E8 mus musculu |
| 18 | 83.5 | 10.3 | 454 | 6 Q8HZU7 | Q8HZU7 tonatia sau |
| 19 | 83.5 | 10.3 | 454 | 6 Q8HZU6 | Q8HZU6 tonatia sau |
| 20 | 83.5 | 10.3 | 454 | 6 Q8HZU5 | Q8HZU5 tonatia sau |
| 21 | 83 | 10.2 | 376 | 11 Q8JZN0 | Q8JZN0 mus musculu |
| 22 | 82 | 10.1 | 263 | 3 Q74316 | Q74316 schizosacch |
| 23 | 82 | 10.1 | 1534 | 5 Q8MPV7 | Q8MPV7 caenorhabdi |
| 24 | 81.5 | 10.0 | 599 | 5 Q8I2G6 | Q8I2G6 plasmodium |
| 25 | 81.5 | 10.0 | 617 | 5 Q25986 | Q25986 plasmodium |
| 26 | 81.5 | 10.0 | 1049 | 2 Q93KF0 | Q93KF0 caldicellul |
| 27 | 80.5 | 9.9 | 825 | 5 Q8IC17 | Q8IC17 plasmodium |
| 28 | 80.5 | 9.9 | 866 | 16 Q84500 | Q84500 chlamydia t |
| 29 | 79.5 | 9.8 | 595 | 10 Q9SDM4 | Q9SDM4 dunaliella |
| 30 | 79.5 | 9.8 | 1044 | 3 Q94173 | Q94173 pneumocysti |
| 31 | 79 | 9.7 | 452 | 16 Q25249 | Q25249 helicobacte |
| 32 | 79 | 9.7 | 10578 | 5 Q8ISF5 | Q8ISF5 caenorhabdi |
| 33 | 79 | 9.7 | 18519 | 5 Q8ISF6 | Q8ISF6 caenorhabdi |
| 34 | 79 | 9.7 | 18534 | 5 Q8ISF7 | Q8ISF7 caenorhabdi |
| 35 | 78.5 | 9.7 | 204 | 2 Q9ZJ7 | Q9ZJ7 clostridium |
| 36 | 78.5 | 9.7 | 1061 | 16 Q8DU02 | Q8DU02 streptococ |
| 37 | 78 | 9.6 | 261 | 16 Q8CU21 | Q8CU21 staphylococ |
| 38 | 78 | 9.6 | 277 | 16 Q8DU44 | Q8DU44 streptococ |
| 39 | 78 | 9.6 | 473 | 5 Q16673 | Q16673 caenorhabdi |
| 40 | 78 | 9.6 | 2578 | 5 Q8IJ99 | Q8IJ99 plasmodium |
| 41 | 77.5 | 9.5 | 454 | 6 Q8HZU4 | Q8HZU4 tonatia bid |
| 42 | 77.5 | 9.5 | 454 | 6 Q8HZU3 | Q8HZU3 tonatia bid |
| 43 | 77.5 | 9.5 | 454 | 6 Q8HZU2 | Q8HZU2 tonatia bid |
| 44 | 77.5 | 9.5 | 1251 | 13 Q91365 | Q91365 coturnix co |
| 45 | 77 | 9.5 | 364 | 16 Q9PM33 | Q9PM33 campylobact |

ALIGNMENTS

RESULT 1

Q96KJ8 ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 4; Length 193;
Best Local Similarity 97.5%; Pred. No. 5e-71; Indels 0; Gaps 0;
Matches 153; Conservative 2; Mismatches 2;

| | | | |
|----|-----|---|-----|
| Qy | 1 | YFGKLESKLSVIRNLNDQVLFDQGNRPDPEDMTDSCDRNAPRTIFIIISMYKDSQPRGM | 60 |
| Db | 37 | YFGKLESKLSVIRNLNDQVLFDQGNRPDPEDMTDSCDRNAPRTIFIIISMYKDSQPRGM | 96 |
| Qy | 61 | AVTISVCEKISKLSKSCNKIISPKEMPPONIKTKSDIIPFQSVGHQNDKMFESSY | 120 |
| Db | 97 | AVTISVCEKISTLSKCNKIISPKENVPPONIKTKSDIIPFQSVGHQNDKMFESSY | 156 |
| Qy | 121 | EGYFLACEKERDLPKILKKEDELGDRSIMFTVQNE | 157 |
| Db | 157 | EGYFLTCEKERDLPKILKKEDELGDRSIMFTVQNE | 193 |

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RESULT 2
Q9BGIS PRELIMINARY; PRT; 193 AA.
AC Q9BG15; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Interleukin-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2129850; PubMed=11331040;
RA Glavetoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication."
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 97.5%; Score 792; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 2e-70; Indels 0; Gaps 0;
Matches 150; Conservative 5; Mismatches 2;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIINMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNQFESSY 120
DB 97 AVAISVKCEKISTLSKSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 3
Q9MZL8 PRELIMINARY; PRT; 178 AA.
AC Q9MZL8; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney, Liver, and Blood;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 6; Length 178;
Best Local Similarity 77.1%; Pred. No. 7.7e-57;

RESULT 4
Q9GL09 PRELIMINARY; PRT; 193 AA.
AC Q9GL09; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of ovine interleukin 18 cDNA";
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401033; CAC0326.2; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCDOA329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 3.3e-56;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSCSDNAPQTIFIIMYKDSLTRGL 96
QY 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIDKTSDIIFQORSVPGHDKNQFESSY 120
DB 97 AVTISVQCKMSTLSKSCENKIISFKEMNPPDNIDNEGSDIIFQORSVPGHDDKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACKKENDLFKLILKQDDNRDKSIMFTVQNN 193

RESULT 5
Q9SM33 PRELIMINARY; PRT; 192 AA.
AC Q9SM33; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interferon-gamma inducing factor.
GN IGIF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
RT "Nucleotide sequence of feline IGIF cDNA (provisional).";

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RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13923; CAC42918.1; -.
SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 78.1%; Score 634; DB 6; Length 192;
Best Local Similarity 76.4%; Pred. No. 7.9e-55;
Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 60
DB 36 YFGKLEHLKLSIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 95
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNQFESSY 120
DB 96 AVTISVQCKKSTLSCNKNKLSFKEMSPEDNIDSGNDIIFQFQSVPGHDKNQFESSLY 155
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 156 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKN 192

RESULT 6

Q9N1P7 PRELIMINARY; PRT; 192 AA.
AC Q9N1P7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin-18.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1] SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20356335; PubMed=10901174;
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
RT "Cloning, sequencing, and expression of porcine interleukin-18 in
RT Escherichia coli";
RL Mol. Cells 10:343-347 (2000).
DR EMBL; AF196949; AAF35169.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 77.1%; Score 626; DB 6; Length 192;
Best Local Similarity 73.9%; Pred. No. 4.9e-54;
Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 60
DB 36 YFGKLEPKLSIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 95
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNQFESSY 120
DB 96 AVTISVQCKKSTLSCNKNKLSFKEMSPEDNIDSGNDIIFQFQSVPGHDKNQFESSLY 155
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 156 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKN 192

RESULT 7

Q91266 PRELIMINARY; PRT; 196 AA.
AC Q91266;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin 18.
OS Sigmodon hispidus (Hispid cotton rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1] SEQUENCE FROM N.A.
RP Blanco J.C., Platneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 196 AA; 22545 MW; E27CSBDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 9.4e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;
QY 2 FKGLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 60
DB 39 PFKESSTAVIRNMNDVYLFIDREKSPVFEDMPDADQKANEATRLIIMYKTDNPGGL 98
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNQFESSY 120
DB 99 PVTLSVRDRTMRTLSCKNQIISPEMDPPLBIDGKSDLIFFQRAVPGH-NMKFESSLH 157
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVON 155
DB 158 EGFFLACEKERDGSFLKILKKEDELGDRSIMFTVTN 192

RESULT 8

Q95LE7 PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1] SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-
RT PCR";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327900; AAL26920.1; -.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.6e-23;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 60
DB 5 YFGKLEPKLSIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKQSPRGM 64
QY 61 AVTISVKCEKISXLSKCNK 79
DB 65 AVTISVKYKTMSTLSCNKN 83
RESULT 9
Q9NQ49 PRELIMINARY; PRT; 45 AA.
ID Q9NQ49
AC Q9NQ49;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -.
FT NON_TER 1
FT NON_TER 45
FT NON_TER 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.7e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 39
Db 7 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 45

RESULT 10
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC6358211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 3.2e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RG 59
Db 43 FSKEKTLHRLNRVNSQLVVRPDLNMAAFEDVTDQEMKSGGWN-FCHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISXLSCEKN-----IISFKEMNPPDNIKDTSDIIFQFORSVPGHDNK-M 113
Db 102 MPVAFSVRVEDKSYVMCCBEHCKMIVRPREGEVPKDIPG-ESNIFFKFTTSYSSKAF 160

QY 114 QFESSSYEGYFLACEKRDLFKLILKK---EDELGDRSIMFTVQNE 156
Db 161 KFEYSLEGRMGFLAFEEEDSLRKLILKLKLPREDEVDETTITLTSRNE 207

RESULT 11
ID Q9AV26 PRELIMINARY; PRT; 198 AA.
AC Q9AV26;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin-18 precursor (Fragment).
GN IL-18.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22195503; PubMed=12206831;
RT "Turkey and chicken interleukin-18 (IL18) share high sequence
RT identity, but have different polyadenylation sites in their 3' UTR.";
RL Dev. Comp. Immunol. 26:681-687(2002).
DR EMBL; AJ312000; CAC83483.1; -.
KW Signal.
FT NON_TER 1
FT NON_TER 28
FT SIGNAL <1
FT CHAIN 29
FT CHAIN 198
SQ SEQUENCE 198 AA; 22967 MW; A1D450BC7207BFAD CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;
Best Local Similarity 34.9%; Pred. No. 2.1e-10;
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RG 59
Db 31 FCKEKTIKLFRNVNSQLVVRPDLNMAAFEDVTDQEVKSGS-GMYFDIHCYKTTAPSAG 89

QY 60 MAVTISVKCEKISXLSCEKN-----IISFKEMNPPDNIKDTSDIIFQFORSVPGHDNK-M 113
Db 90 MPVAFSVQVEDKSYVMCCBEHCKMIVRPREGEVPKDIPG-ESNIFFKFTTSYSSKAF 148

QY 114 QFESSSYEGYFLACEKRDLFKLILKK---EDELGDRSIMFTVQNE 156
Db 149 KFEYSLEQGMFLAFEEEDSLRKLILKLKLPREDEVDETTITKFTSRNE 194

RESULT 12
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20508574; PubMed=11054275;
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883 (2000).
DR EMBL; AJ277865; CAB96214.1; -.
FT CHAIN 30
FT CHAIN 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 3.2e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RGMVATISVKCEK 70
Db 42 RNVNSQLVVRPDLNMAAFEDVTDQEVKSGS-GMYFDIHCYKTTAPSAGMPVAFSQQVED 100

QY 71 ISKLSCEKN-----IISFKEMNPPDNIKDTSDIIFQFORSVPGHDNK-MQFESSSYEGYF 124
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| | |
|--------------------------------|--|
| RA | Brinton M.A.; |
| RT | "Positional cloning of the murine flavivirus resistance gene."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:9322-9327(2002). |
| DR | EMBL; AF418009; AAM47549.1; -. |
| DR | MGD; MGI:97430; Oaslb. |
| DR | InterPro; IPR006117; 25A_SYNTH_2. |
| DR | InterPro; IPR006116; 25A_synth_UB. |
| DR | InterPro; IPR001201; PAP_25A_core. |
| DR | PROSITE; PS00833; 25A_SYNTH_2; 1. |
| DR | PROSITE; PS0152; 25A_SYNTH_3; 1. |
| SQ | SEQUENCE 376 AA; 43642 MW; 5807F6EE436FCA26 CRC64; |
| | |
| Query Match | 10.7%; Score 86.5; DB 11; Length 376; |
| Best Local Similarity | 23.3%; Pred.No.2; |
| Matches | 40; Conservative 28; Mismatches 65; Indels 39; Gaps 7 |
| | |
| Qy | 5 LESKLSVIRNLNDQVLFDIQGNRPLFPEDMTDSDCRDNAPTIFILISMVKDQSPRCMAVTI 64 |
| Dd | 59 VKGCKTALKGRSDADLVFLNNLTYPEDQLNQ-----QGVLKEIKKKLYEVQHERRF 111 |
| Qy | 65 SVKCEKISXLSCEKNKIISFKEMNPDPNIKOTKSDII-----PFG---- 103 |
| Dd | 112 GVRFVEVSQRSNSRALSPFK-LSAPDLLKVEKFDVLPAYDLDDHLNLLKKPNQPFYANLI 170 |
| Qy | 104 --RSVPGHNDNMQPSSSYGYFIACE--KERDLFKLI-----LKKEDELGD 146 |
| Dd | 171 SGRTPPGKEGLSICFMGLAKRYFLNCRPTKLRLIRLIVTHWYQLCKE-KLGD 221 |
| | |
| RESULT 15 | |
| ID | Q8JZN4 PRELIMINARY; PRT; 252 AA. |
| QID | Q8JZN4; 22, Created) |
| AC | 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) |
| DT | 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) |
| DE | 2'-5' oligoadenylate synthetase 1B (2'-5'-oligoadenylate synthetase |
| DE | 1). |
| OS | OAS1A OR OAS1B OR OAS1. |
| OC | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C3H/He. |
| RX | MEDLINE=22103633; PubMed=12080145; |
| RA | Pereleygin A.A.; Scherblk S.V., Zhulin I.B., Stockman B.M., Li Y., |
| RT | "Positional cloning of the murine flavivirus resistance gene."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:9322-9327(2002). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=BALB/c; |
| RX | MEDLINE=22177231; PubMed=12186974; |
| RA | Mashimo T., Lucas M., Simon-Chazottes D., Frenkiel M.P., |
| RA | Montagutelli X., Ceccaldi P.E., Deubel V., Guenet J.L., Despres P.; |
| RT | "A nonsense mutation in the gene encoding 2'-5'-oligoadenylate |
| RT | synthetase/L1 isoform is associated with West Nile virus |
| RT | susceptibility in laboratory mice."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:11311-11316(2002). |
| ENBL; AF418004; AAM47544.1; -. | |
| DR | EMBL; AF466822; AAM97603.1; -. |
| DR | MGD; MGI:2180860; Oasla. |
| DR | MGD; MGI:97430; Oaslb. |
| DR | InterPro; IPR006116; 25A_synth_UB. |
| DR | InterPro; IPR001201; PAP_25A_core. |
| DR | PROSITE; PS0152; 25A_SYNTH_3; 1. |
| SQ | SEQUENCE 252 AA; 28812 MW; 552108B5041006CD CRC64; |
| | |
| Query Match | 10.5%; Score 85; DB 11; Length 252; |
| Best Local Similarity | 23.1%; Pred.No.1.8; |
| Matches | 42; Conservative 25; Mismatches 49; Indels 66; Gaps 8 |

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Qy 3 GKLESKLSVIRN-----LNDQVLFIDQGNRELFEDMTDSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVVFLNNLTSPFEDQLNQGVLIKEIKQKQCEVQHERRC----- 111
Qy 55 SQPRGMATISVCKEIKSXLSCENKIISFKEMNPPDNIKDTKSDII----- 100
Db 112 -----GVKPEVHSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLIK 160
Qy 101 -----FFQ-----RSVPGHDNKMQFESSSYEGYFLACE--KERDLFKLI-----LKKED 144
Db 161 PNOQFYANLISGRTPPGKEGKLSICFMGLQKYLNCRPTKIKRLIRLVTHWYQCKE-KL 219
Qy 145 GD 146
Db 220 GD 221
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Search completed: December 12, 2003, 17:53:42
Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:46:35 ; Search time 42 Seconds
(without alignments)
593.335 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LKDELDGDRSIMFTVQNEQ 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------------|
| 1 | 811 | 99.9 | 157 | 19 | AAW77077 Human interleukin |
| 2 | 811 | 99.9 | 157 | 21 | AAAY5750 Human interleukin |
| 3 | 811 | 99.9 | 157 | 22 | AAE05661 Human interleukin |
| 4 | 811 | 99.9 | 157 | 22 | AAAG5294 Human interleukin |
| 5 | 811 | 99.9 | 157 | 22 | AAAG5351 Human interleukin |
| 6 | 811 | 99.9 | 157 | 23 | ABE04389 Human IL-18. Homo |
| 7 | 811 | 99.9 | 157 | 23 | AAE16954 Human active inter |
| 8 | 811 | 99.9 | 157 | 23 | AAE17134 Human IL-18 protei |
| 9 | 811 | 99.9 | 157 | 24 | ABG73359 Human wild-type ma |

| | | | | | |
|----|-----|------|------|----|------------------------------|
| 10 | 811 | 99.9 | 158 | 21 | AAAY85167 Human interleukin |
| 11 | 811 | 99.9 | 180 | 19 | AAW48959 Wild-type human in |
| 12 | 811 | 99.9 | 193 | 18 | AAW22047 Interferon gamma i |
| 13 | 811 | 99.9 | 193 | 19 | AAW46592 Amino acid sequenc |
| 14 | 811 | 99.9 | 193 | 22 | AAAB30541 A human IL-18 with |
| 15 | 811 | 99.9 | 193 | 22 | AAAG63830 Amino acid sequenc |
| 16 | 811 | 99.9 | 193 | 23 | AAE16953 Human precursor in |
| 17 | 811 | 99.9 | 233 | 23 | AAE16959 Ubiquitin-human in |
| 18 | 811 | 99.9 | 536 | 23 | AAE16957 Human pro-IL-18/ca |
| 19 | 811 | 99.9 | 588 | 23 | AAE16958 Human pro-IL-18/ca |
| 20 | 811 | 99.9 | 1048 | 23 | AAE16960 Ubiquitin-human in |
| 21 | 810 | 99.8 | 157 | 17 | AAAR99564 Human interferon-g |
| 22 | 810 | 99.8 | 157 | 17 | AAAR99558 Human mature inter |
| 23 | 810 | 99.8 | 157 | 18 | AAWI5701 Interferon-gamma i |
| 24 | 810 | 99.8 | 157 | 18 | AAW24258 Human protein for |
| 25 | 810 | 99.8 | 157 | 19 | AAW77158 Human interleukin- |
| 26 | 810 | 99.8 | 157 | 19 | AAW63810 Human IL-18 protei |
| 27 | 810 | 99.8 | 157 | 19 | AAW37741 IFN-gamma inducing |
| 28 | 810 | 99.8 | 157 | 19 | AAW52176 Interferon-gamma i |
| 29 | 810 | 99.8 | 157 | 20 | AAAY39799 Interleukin-18 rec |
| 30 | 810 | 99.8 | 157 | 21 | AAAY44597 Human interleukin- |
| 31 | 810 | 99.8 | 157 | 21 | AAAY53904 Sequence of a matu |
| 32 | 810 | 99.8 | 157 | 22 | AAAB82408 Human interleukin- |
| 33 | 810 | 99.8 | 193 | 17 | AAAR99560 Human interferon-g |
| 34 | 810 | 99.8 | 193 | 19 | AAW37740 Interferon-gamma i |
| 35 | 810 | 99.8 | 193 | 19 | AAW52172 Interferon-gamma i |
| 36 | 810 | 99.8 | 193 | 19 | AAW47429 Interferon-gamma p |
| 37 | 810 | 99.8 | 193 | 21 | AAAY53908 Amino acid sequenc |
| 38 | 810 | 99.8 | 193 | 22 | AAAB82409 Human interleukin- |
| 39 | 808 | 99.5 | 193 | 19 | AAW77082 Interleukin 18 act |
| 40 | 807 | 99.4 | 157 | 24 | ABG73367 Human mature inter |
| 41 | 807 | 99.4 | 193 | 24 | ABG73366 Human precursor in |
| 42 | 805 | 99.1 | 157 | 24 | ABG73363 Human mature inter |
| 43 | 805 | 99.1 | 157 | 24 | ABG73364 Human mature inter |
| 44 | 805 | 99.1 | 193 | 24 | ABG73360 Human precursor in |
| 45 | 805 | 99.1 | 193 | 24 | ABG73361 Human precursor in |

ALIGNMENTS

RESULT 1

AAW77077
ID AAW77077 standard; peptide; 157 AA.

XX AAW77077;

AC AAW77077;

XX 16-NOV-1998 (first entry)

DT Human interleukin 18.

DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

XX Homo sapiens.

OS EP861663-A2.

PN 02-SEP-1998.

PD 24-FEB-1998; 98EP-0301352.

PF 25-FEB-1997; 97JP-0055468.

PR (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

DR N-PSDB; AAW48226.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment

PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis

XX Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSOPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSOPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120

DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 2

AAV57570

ID AAY57570 standard; protein; 157 AA.

XX AAY57570;

XX 06-MAR-2000 (first entry)

XX Human interleukin 18 protein sequence SEQ ID NO:1.

XX Human; interleukin 18; IL-18; potentiator; IGIF;tumour; cancer;
 XX interferon-gamma-inducing factor; growth inhibition; cytostatic.

XX Homo sapiens.

XX WO9959565-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11160.

XX 21-MAY-1998; 98US-0086560.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johnson RK;

XX WPI; 2000-062368/05.

XX New polypeptides, useful for preparation of composition for preventing
 XX and/or treating cancer by inhibiting tumor growth

PS Claim 1; Page 49-50; 53pp; English.

XX The present sequence represents human interleukin 18 (IL-18). The
 CC present invention describes a compound comprising human or murine IL-18
 CC in combination with a chemotherapeutic agent (I). Also described are:
 CC (1) a method of preventing and/or treating cancer in a mammal comprising
 CC the administration of a cancer inhibiting amount of (I) comprising the
 CC IL-18 protein and the chemotherapeutic agent and optionally a
 CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the

CC growth of tumour cells in a mammal sensitive to a composition comprising
 CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
 CC optionally a pharmaceutically acceptable carrier), comprising
 CC administering to a mammal afflicted with the tumour cells an effective
 CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
 CC conjunction with a chemotherapeutic agent is useful in a method for
 CC preventing and/or treating cancer in mammals by inhibiting the growth
 CC of tumours or cancerous cells in mammals.

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 21; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSOPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSOPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120

DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3

AAE06661

ID AAE06661 standard; Protein; 157 AA.

XX AAE06661;

XX 16-OCT-2001 (first entry)

XX Human interleukin-1gamma (IL-1gamma) protein.

XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
 XX immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 XX autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 XX psoriasis; viral infection; allergy; cytokine; HIV; drug screening.

XX Homo sapiens.

XX WO200157219-A2.

XX 09-AUG-2001.

XX 01-FEB-2001; 2001WO-US03285.

XX 02-FEB-2000; 2000US-0179638.

XX (SCHE) SCHERING CORP.

XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;

XX WPI; 2001-488886/53.

XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal
 PT expression of interleukin such as immunological disorders, tumor and
 PT allergy

PS Disclosure; Fig 1; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1gamma (IL-1gamma) protein related to the invention.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Qy 61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHDNMQPFESSY 120
 Db 61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHDNMQPFESSY 120
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
 AAG65294
 ID AAG65294 standard; protein; 157 AA.
 XX
 AC AAG65294;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 FN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 9; 91pp; English.
 XX
 The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The

CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Qy 61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHDNMQPFESSY 120
 Db 61 AVTISVKCEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHDNMQPFESSY 120
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
 AAG65351
 ID AAG65351 standard; protein; 157 AA.
 XX
 AC AAG65351;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 FN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 14; 91pp; English.
 XX
 The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 protein fragment.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 6
ID ABB04389 standard; protein; 157 AA.
XX ABB04389;
XX ABB04389;
DT 21-MAY-2002 (first entry)
XX Human IL-18.
DE Human; IL-18; interleukin-18; cancer.
KW Homo sapiens.
OS CN1326992-A.
PN 19-DEC-2001.
PD 07-JUN-2000; 2000CN-0107993.
PF 07-JUN-2000; 2000CN-0107993.
PR (SHUA-) SHUANGU PHARM CO LTD BEIJING.
PA Xu M, Wang Y, Huang X;
XX WPI; 2002-217571/28.
XX N-PSDB; ABL41315.
DR Gene cloning, product preparation and use of Chinese interleukin-18
PT subtype (53 Arg IL-18), useful for treating of cancer and other disease
PT Claim 1; Page 7 (Disclosure); 8pp; Chinese.
XX The invention relates to the preparation of recombinant human
CC interleukin-18 for treating of cancer and other disease.
XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
ID AAE16954 standard; Protein; 157 AA.
XX AAE16954;
AC AAE16954;
XX 18-APR-2002 (first entry)
DT Human active interleukin-18 (IL-18) protein.
XX Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;
KW immunocompetent.
XX Homo sapiens.
OS WO200198455-A2.
PN 27-DEC-2001.
PD 11-JUN-2001; 2001WO-US18804.
PF 15-JUN-2000; 2000US-211832P.
PR 10-AUG-2000; 2000US-224128P.
PR 20-JAN-2001; 2001US-264923P.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Johanson KO, Kirkpatrick RB, Shatzman AR, Ho YS, Mcdevitt P;
PI WPI; 2002-139786/18.

XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide
PT useful for inducing interferon-gamma production, comprises contacting
PT or co-expressing caspase 4 or caspase 5 with precursor polypeptide -
XX Claim 9; Fig 3; 64pp; English.
XX The invention relates to a method for the in vitro activation of human
CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
CC method comprises contacting precursor IL-18 with an activating enzyme
CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
CC of cysteine proteases that include interleukin-beta converting enzyme
CC (ICE), which preferentially cleave substrates containing a protease
CC activation motif. The methods are useful for producing physiologically
CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18
CC polypeptide has an activity of inducing the production of interferon
CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
CC biologically active substance for stimulating the production of IFN-gamma
CC from KG-1 (human myelomonocytic cell line) cells. The present sequence
CC is human active IL-18 protein.
XX Sequence 157 AA;
SQ Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;

| | | | |
|----|-----|--|-----|
| Db | 61 | AVTISVCKEITSLSCENKIISPKEMNPPDINKOTKSDIIFQRSVPGHDKMQPSSSY | 120 |
| Qy | 121 | EGYFLACEKERDLPKILKKEDELGDRSMFTVNQED | 157 |
| Db | 121 | EGYFLACEKERDLPKILKKEDELGDRSMFTVNQED | 157 |

RESULT 9
ABG73359
ID ABG
XX
AC ABG

13-MAY-2003 (FIRST ENTRY)
Human wild-type mature interleukin-18 (IL-18).

Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP; T helper type I response; Th1 response; cancer; viral disease; microbial infection; tumour immunotherapy; adjuvant; DNA vaccination; graft versus tumour therapy; neutralisation; cytostatic; virucide; antimicrobial.

antimicrobial:
Homo sapiens.

08-MAR-2002; 2002US-0094153.
08-MAR-2001; 2001US-274327P.

(DINA//) DINARELLO C.
(KIMS//) KIM S H.

(KIMS//) KIM S H.

Dinarello C, Kim SH

WPI; 2003-298731/29.
N-PSDB: ABX11788.

Novel interleukin-18

cancer and viral diseases are involved in its

Example 1: Fig 1B: 2

The present invention

(IL-18) protein that protein (IL-18BP) th

mutants of the inven-
acid residues which

The mutations comprising additions or deletions

IL-18 mutant is used alleviated by a the

and viral disease. The above diseases.

and as an adjuvant in the IL-18 therapy. The IL-18 m

neutralisation than represents human will

Sequence 157 AA:

rv Match

t Local Similarity
ches 156: Conserva

1 YFGKLESKLSV

1 YFGKLESKLSV

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157

RESULT 10

AAV85167
ID AAV85167 standard; Protein; 158 AA.
XX AC AAV85167;
XX XX 23-JUN-2000 (first entry)
XX DE Human interleukin-18 (IL-18) amino acid sequence.
XX KW Interleukin-18; production; IL-18; human; medical injection product.
XX OS Homo sapiens.
XX XX CN1243130-A.
XX PN 02-FEB-2000.
XX PD 24-JUL-1998; 98CN-0103307.
XX PF 24-JUL-1998; 98CN-0103307.
XX PR 24-JUL-1998; 98CN-0103307.
XX PA (WUGG/) WU G.
XX PI Wu G, Liu Z;
XX DR WPI; 2000-340020/30.
XX DR N-PSDB; AAA10526.
XX XX Preparation method for engineering bacteria for recombination of human
PT interleukin-18 and its product thereof -
XX Claim 1; Page 2; 17pp; English.

XX This sequence represents the human interleukin-18 (IL-18) amino acid
CC sequence. The invention relates to a method for engineering bacterium for
CC recombination of human IL-18 and a method for the preparation of IL-18. A
CC primer containing a restriction endonuclease site can be used to.
CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
CC stop codon preferred by coli bacillus to raise the expression rate. The
CC method uses a high-amplification culture medium to increase the
CC expression level and only requires a one-step purification process to
CC obtain a medical injection-pure product.

XX Sequence 158 AA;

Query Match 99.9%; Score 811; DB 21; Length 158;
Best Local Similarity 99.4%; Pred. No. 8.3e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 61

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
DB 62 AVTISVKCEKISTLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 121

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157
DB 122 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 158

RESULT 11

AAW48959
ID AAW48959 standard; Peptide; 180 AA.
XX AC AAW48959;
XX XX 25-SEP-1998 (first entry)
XX DE Wild-type human interferon-gamma inducing factor.
XX KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX XX
XX PH Key
XX FT Peptide
XX FT Protein
XX FT /note= "signal peptide"
XX FT /note= "Mature human IGIF which is claimed by the
XX FT /note= "inventors under claim 3 in the specification"
XX PN EP845530-A2.
XX XX 03-JUN-1998.
XX XX 28-NOV-1997; 97EP-0309632.
XX PR 14-NOV-1997; 97JP-0329715.
XX PR 29-NOV-1996; 96JP-0333037.
XX PR 21-JAN-1997; 97JP-0020906.
XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX XX Kurimoto M, Okamoto I, Yamamoto K;
XX PI WPI; 1998-288747/26.
XX DR N-PSDB; AAV32754.
XX XX Mutants of interferon-gamma inducing polypeptide - useful as
PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX Claim 3; pages 36-37; 59pp; English.

XX The present sequence represents the wild-type human interferon-gamma
CC inducing factor (IGIF). The invention provides for mutant human and
CC mouse interferon-gamma inducing factors in which one or more cysteine
CC residues are replaced with different residues at or away from the
CC consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
CC capable of stimulating immunocompetent cells for the production of
CC interferon-gamma and are claimed to be less toxic, more active and
CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
CC formation, and may therefore be useful as antitumour agents, antitumour
CC immunotherapeutics, antiviral agents and antimicrobial agents. The
CC mutant IGIFs are also claimed to be useful for treating hepatitis, solid
CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, and
CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
CC thrombopenia caused by radiation- and chemo-therapy.

XX Sequence 180 AA;

Query Match 99.9%; Score 811; DB 19; Length 180;

Best Local Similarity 99.4%; Pred. No. 9.9e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60

DB 24 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 83

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120

157 EGYFLACBKERDLFXILKKDELGDRSIMPTQVND 193

RESULT 13
AAW46592
ID AAW46592 standard; Protein; 193 AA.
XX
XX AAW46592;
XX
XX 21-MAY-1998 (first entry)
XX
XX Amino acid sequence of human interleukin-1-gamma.
XX
XX Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
XX induction; antibody; diagnostic assay; fusion protein; activity;
XX immunological disorder; allergy.
XX
XX Homo sapiens.
XX
XX
XX Location/Qualifiers
XX 41..47
XX Region /note= "beta-1 region"
XX
XX 55..59
XX Region /note= "beta-2 region"
XX
XX 64..68
XX Region /note= "beta-3 region"
XX
XX 83..88
XX Region /note= "beta-4 region"
XX
XX 96..102
XX Region /note= "beta-5 region"
XX
XX 108..113
XX Region /note= "beta-6 region"
XX
XX 115..120
XX Region /note= "beta-7 region"
XX
XX 137..143
XX Region /note= "beta-8 region"
XX
XX 147..153
XX Region /note= "beta-9 region"
XX
XX 160..164
XX Region /note= "beta-10 region"
XX
XX 170..175
XX Region /note= "beta-11 region"
XX
XX 187..191
XX Region /note= "beta-12 region"
XX
XX
XX WO9744468-A1.
XX
XX 27-NOV-1997.
XX
XX 16-MAY-1997; 97WO-US07282.
XX
XX 20-MAY-1996; 96US-0651998.
XX
XX (SCHE) SCHERING CORP.
XX
XX Bazan JF, Hardiman GT, Kastelein RA, Sana TR, Timans JC;
XX
XX WPI; 1998-018522/02.
XX
XX N-PSDB; AAV05368.
XX
XX Antagonist of human interleukin-1-gamma - used for treating
XX immunological disorders caused by human IL-1-gamma
XX
XX Disclosure; Pages 54-55; 63pp; English.
XX
XX The present sequence represents human interleukin-1-gamma (IL-1-gamma).
XX The protein is the human equivalent of a mouse cytokine, IGIF, which
XX induces certain T cells to produce interferon-gamma. Human IL-1-gamma
XX and mouse IGIF show 71% identity at the nucleotide level and
XX approximately 65% identity at the amino acid level. Antagonists of
XX IL-1 gamma, e.g. antibodies, can be used in a method for treating a
XX condition caused by human IL-1 gamma. The antibodies can also be used

CC in diagnostic assays. The IL-1-gamma protein can be covalently
CC conjugated to polyethylene glycol or to a polypeptide, and the fusion
CC protein used in a pharmaceutical composition for supplying the
CC biological activity of IL-1 gamma. Conditions that can be treated using
CC the human IL-1-gamma protein include immunological disorders, allergies,
CC and infectious diseases. The IL-1-gamma can also be used to detect the
CC presence of the protein or its receptor.

XX SQ Sequence 193 AA;

Query Match 99.9%; Score 811; DB 19; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSOPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSOPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKENMPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKENMPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 193

RESULT 14

AAB30541
ID AAB30541 standard; Protein; 193 AA.

XX AC AAB30541;

XX DT 06-MAR-2001 (first entry)

XX DE A human IL-18 with a caspase-8 cleavage site.

XX KW Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT FT Cleavage-site 33..36
FT FT /note= "caspase-8 cleavage site"

PN WO200061768-A2.

XX 19-OCT-2000.

XX PF 13-APR-2000; 2000WO-IL00220.

XX PR 13-APR-1999; 99IL-0129427.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;

XX DR WPI; 2001-006910/01.

XX DR N-PSDB; AAC62200.

XX PT Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule

PS Disclosure; Fig 8a-b; 40pp; English.

XX CC The present sequence represents a human pro interleukin-18 (IL-18).

XX CC with a caspase-8 cleavage site. The natural cleavage site of IL-18

XX CC was mutated to a site susceptible to cleavage by a common protease.

XX CC The specification describes a method for the preparation of biologically

XX CC active molecules from their biologically inactive precursors. The method

CC comprises mutating the native cleavage site to a site capable of being
CC cleaved by a protease and cleaving the mutated molecule to yield the
CC active compound. The method is especially used to produce active
CC cytokines, such as IL-18.

XX SQ Sequence 193 AA;

Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSOPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSOPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKENMPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKENMPDNIKDTKSDIIFQORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNEED 193

RESULT 15

AAG63830
ID AAG63830 standard; Protein; 193 AA.

XX AC AAG63830;

XX DT 26-NOV-2001 (first entry)

XX DE Amino acid sequence of human interleukin 18 (IL-18).

XX KW T-cell-helper type 2 response; Th2 response; T cell mediated response;

XX KW allergic response; interleukin 18; IL-18; IGE-mediated allergy;

XX KW allergic asthma; anaphylactic reaction; asthma associated allergy;

XX KW IGE dependent allergic rhinoconjunctivitis.

XX OS Homo sapiens.

XX PN WO200168896-A1.

XX PD 20-SEP-2001.

XX PF 02-MAR-2001; 2001WO-US06869.

XX PR 10-MAR-2000; 2000US-0188311.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX PI Levy S, Dekruyff RH, Umetsu DT, Maecker H;

XX DR WPI; 2001-570874/64.

XX DR N-PSDB; AAH78060.

XX PT Reducing antigen specific immune response in conditions such as asthma,
XX PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
XX PT antigen-specific allergic response -

XX PS Disclosure; Page 36; 38pp; English.

XX CC The specification describes a method for reducing a T-cell-helper

XX CC type 2 (Th2) T cell mediated antigen-specific allergic response. The

XX CC method comprises administering a DNA construct encoding a fusion

XX CC protein of interleukin 18 (IL-18) and an antigen associated with the

XX CC allergic response. The method is useful for reducing a Th2 T cell

XX CC mediated antigen-specific allergic response especially IGE-mediated

XX CC allergic asthma or anaphylactic reactions or IGE dependent allergic

XX CC rhinoconjunctivitis, and for treating asthma associated allergies where

XX CC the allergies are ongoing at the time of the administration. The

XX CC present sequence represents a human IL-18, and is used to construct

XX CC fusion proteins of the invention.


```
XX SQ Sequence 193 AA;
Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred No. 1,1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPCHDNKMQFESSY 120
Db 97 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPCHDNKMQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
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Search completed: December 12, 2003, 17:52:26
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:41:24 ; Search time 21 Seconds
(without alignments)
316.324 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 811 | 99.9 | 157 | 4 | US-08-982-285-4 |
| 2 | 811 | 99.9 | 157 | 4 | US-09-700-609-1 |
| 3 | 810 | 99.8 | 157 | 2 | US-08-896-605A-6 |
| 4 | 810 | 99.8 | 157 | 2 | US-08-896-501A-4 |
| 5 | 810 | 99.8 | 157 | 3 | US-08-884-324-1 |
| 6 | 810 | 99.8 | 157 | 3 | US-08-996-338-26 |
| 7 | 810 | 99.8 | 157 | 3 | US-08-558-818-1 |
| 8 | 810 | 99.8 | 157 | 3 | US-08-974-469A-1 |
| 9 | 810 | 99.8 | 157 | 3 | US-08-832-180-1 |
| 10 | 810 | 99.8 | 157 | 3 | US-08-832-198-6 |
| 11 | 810 | 99.8 | 157 | 4 | US-09-819-902-6 |
| 12 | 810 | 99.8 | 157 | 4 | US-09-752-510-6 |
| 13 | 810 | 99.8 | 157 | 4 | US-09-711-899-1 |
| 14 | 810 | 99.8 | 157 | 4 | US-09-556-972-26 |
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| 16 | 810 | 99.8 | 193 | 2 | US-08-896-501A-2 |
| 17 | 810 | 99.8 | 193 | 3 | US-08-832-180-9 |
| 18 | 801 | 98.6 | 157 | 4 | US-08-982-285-6 |
| 19 | 792 | 97.5 | 193 | 4 | US-09-597-576-2 |
| 20 | 791 | 97.4 | 157 | 4 | US-08-982-285-7 |
| 21 | 791 | 97.4 | 157 | 4 | US-08-982-285-8 |
| 22 | 782 | 96.3 | 157 | 4 | US-08-982-285-11 |
| 23 | 781 | 95.2 | 157 | 4 | US-08-982-285-9 |
| 24 | 772 | 95.1 | 157 | 4 | US-08-982-285-12 |
| 25 | 771 | 95.0 | 157 | 4 | US-08-982-285-10 |
| 26 | 517 | 63.7 | 157 | 4 | US-08-982-285-13 |
| 27 | 515 | 63.4 | 157 | 4 | US-08-982-285-5 |

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| 28 | 515 | 63.4 | 157 | 4 | US-09-700-609-2 | Sequence 2, Appli |
| 29 | 513 | 63.2 | 157 | 2 | US-08-502-535B-2 | Sequence 2, Appli |
| 30 | 513 | 63.2 | 157 | 2 | US-08-908-005A-2 | Sequence 2, Appli |
| 31 | 513 | 63.2 | 157 | 3 | US-08-996-338-27 | Sequence 27, Appli |
| 32 | 513 | 63.2 | 157 | 3 | US-08-558-818-7 | Sequence 7, Appli |
| 33 | 513 | 63.2 | 157 | 3 | US-08-974-469A-7 | Sequence 7, Appli |
| 34 | 513 | 63.2 | 157 | 3 | US-08-832-180-8 | Sequence 8, Appli |
| 35 | 513 | 63.2 | 157 | 3 | US-08-832-198-11 | Sequence 11, Appli |
| 36 | 513 | 63.2 | 157 | 3 | US-09-253-523-2 | Sequence 2, Appli |
| 37 | 513 | 63.2 | 157 | 3 | US-09-251-911-2 | Sequence 2, Appli |
| 38 | 513 | 63.2 | 157 | 4 | US-09-819-902-11 | Sequence 11, Appli |
| 39 | 513 | 63.2 | 157 | 4 | US-09-752-510-11 | Sequence 11, Appli |
| 40 | 513 | 63.2 | 157 | 4 | US-09-711-899-7 | Sequence 7, Appli |
| 41 | 513 | 63.2 | 157 | 4 | US-09-556-972-27 | Sequence 27, Appli |
| 42 | 505 | 62.2 | 157 | 4 | US-08-982-285-14 | Sequence 14, Appli |
| 43 | 259 | 31.9 | 50 | 3 | US-08-832-198-2 | Sequence 2, Appli |
| 44 | 259 | 31.9 | 50 | 4 | US-09-819-902-2 | Sequence 2, Appli |
| 45 | 259 | 31.9 | 50 | 4 | US-09-752-510-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-08-982-285-4
; Sequence 4, Application US/08982285
; Patent No. 6476197
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Koza
; APPLICANT: OKAMOTO, Iwao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/982,285
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. 6476197ember 29, 1996
; APPLICATION NUMBER: JP 20,906/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. 6476197ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQRSVPGHDNKMOPESSY 120
Db 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQRSVPGHDNKMOPESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakui TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQRSVPGHDNKMOPESSY 120
Db 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQRSVPGHDNKMOPESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakui
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masahi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-DEC-1997
; APPLICATION NUMBER: US/08/996,338
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| 1 | YGKLEKLSVIRNLNDQVLFIDQGNRPPLFEDMTDS | CRDNAPRTFIISMYKDSQPRGM | 60 |
| | | | |
| 61 | AVTISVKEKISXLSCENKIISFKEMPPDNIKTKSDI | IFFQRSVPGHDKNKQFESSY | 120 |
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| 61 | AVTISVKEKISXLSCENKIISFKEMPPDNIKTKSDI | IFFQRSVPGHDKNKQFESSY | 120 |
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| 121 | EGYFLACKEKRDLPKLIILKKGEIDGDRSIMFTVQ | NE | 157 |
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| 121 | EGYFLACKEKRDLPKLIILKKGEIDGDRSIMFTVQ | NE | 157 |
| | | | |

RESULT 7
US-08-558-818-1
; Sequence 1, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

| | Query Match | 99.8% | Score 810; | DB 3; | Length 157; |
|----|-----------------------|--|--------------------|-----------|-------------|
| | Best Local Similarity | 100.0%; | Pred. No. 4.2e-88; | | |
| | Matches 157; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | YFGKLESKLSVIRNLNDQVLFIQGNRPLFEDMTSDCRDNAPRTIIFISMYKDSQPRGM | 60 | | |
| Db | 1 | YFGKLESKLSVIRNLNDQVLFIQGNRPLFEDMTSDCRDNAPRTIIFISMYKDSQPRGM | 60 | | |
| Qy | 61 | AVTISVKCEKISKLSCENKIISPKEMPPNIDTKSDIIFPORSVPGHNKKQPFESSY | 120 | | |
| Db | 61 | AVTISVKCEKISKLSCENKIISPKEMPPNIDTKSDIIFPORSVPGHNKKQPFESSY | 120 | | |

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121 EGYFLACEKRDJFKLILKKEDELGDRSIMFTVQNEED 157
|||||
121 EGYFLACEKRDJFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Steet N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE:
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-469A-1

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| | Query Match | 99.8%; Score 810; DB 3; Length 157; |
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| | Best Local Similarity | 100.0%; Pred. No. 4.2e-88; |
| | Matches 157; Conservative 0; | Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 YFGKLESKLSVLRNLNDQLVFIDQGNRPFLFEDMTDSDCRDNAPRTTIIISMYKDOSPGRGM 60 | |
| Dd | 1 YFGKLESKLSVLRNLNDQLVFIDQGNRPLFEDMTDSDCRDNAPRTTIIISMYKDOSPGRGM 60 | |
| Qy | 61 AVTIISYVCBKIKSLSCENKIIFSPKENNPDPNIKDTKSIIFFORSVPGHDKNKMFESSSY 120 | |
| Dd | 61 AVTIISYVCBKIKSLSCENKIIFSPKENNPDPNIKOTKSIIFFORSVPGHDKNKMFESSSY 120 | |
| Qy | 121 EGYFLACEKERDLFKLIILKKKEDELGDRSIMFTVVQNED 157 | |
| Dd | 121 EGYFLACEKERDLFKLILLKKEDELGDRSIMFTVVQNED 157 | |

RESULT 9

US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: USHIO, Shimpei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:
; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994
; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-832-180-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHNDKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10

US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitaukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'Ile' or 'Thr'
; US-08-832-198-6

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHNDKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-819-902-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIFFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIFFQRSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
RESULT 12
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIFFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIFFQRSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13
US-09-711-899-1
; Sequence 1, Application US/09711899
; Patent No. 6509449
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; WHICH INDUCES INTERFERON- PRODUCTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,899
; FILING DATE: 13-NO. 6509449-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,818
; FILING DATE: 2000-11-15
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELIC1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-711-899-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14
US-09-556-972-26
; Sequence 26, Application US/09556972
; Patent No. 6559298
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; OKURA, Takao
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
CITY: 419 Seventh Street, N.W., Suite 300
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556.972
FILING DATE: 24-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/996.338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-556-972-26

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

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/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/896,605A
/ FILING DATE: 18 July 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 207,691/1996
/ FILING DATE: 19-JUL-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 156,062/1997
/ FILING DATE: 30-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: TANIMOTO=2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 193 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-896-605A-2

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Query Match          99.8%; Score 810; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.5e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIFIISMVKDSQPRGM 60
   |||||
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIFIISMVKDSQPRGM 96
   |||||

QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 120
   |||||
Db 97 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 156
   |||||

QY 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
   |||||
Db 157 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 193
   |||||

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Search completed: December 12, 2003, 17:47:03
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:45:44 ; Search time 31 Seconds
(without alignments)
941.917 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues
Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 811 | 99.9 | 157 | 10 | US-09-775-046-9 |
| 2 | 811 | 99.9 | 157 | 11 | US-09-030-061-6 |
| 3 | 811 | 99.9 | 157 | 12 | US-10-311-491-3 |
| 4 | 811 | 99.9 | 157 | 14 | US-10-100-057-6 |
| 5 | 811 | 99.9 | 157 | 14 | US-10-094-153-2 |
| 6 | 811 | 99.9 | 157 | 15 | US-10-260-576-4 |
| 7 | 811 | 99.9 | 157 | 15 | US-10-297-136-1 |
| 8 | 811 | 99.9 | 193 | 9 | US-09-798-075-1 |
| 9 | 811 | 99.9 | 193 | 10 | US-09-770-528-8 |
| 10 | 811 | 99.9 | 193 | 12 | US-10-311-491-1 |
| 11 | 811 | 99.9 | 233 | 12 | US-10-311-491-10 |
| 12 | 810 | 99.8 | 157 | 7 | US-08-996-140-1 |
| 13 | 810 | 99.8 | 157 | 10 | US-09-924-099-21 |
| 14 | 810 | 99.8 | 157 | 12 | US-10-349-023-26 |
| 15 | 810 | 99.8 | 157 | 16 | US-10-327-069-1 |

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| 16 | 807 | 99.4 | 157 | 14 | US-10-094-153-10 |
| 17 | 807 | 99.4 | 193 | 14 | US-10-094-153-9 |
| 18 | 805 | 99.1 | 157 | 14 | US-10-094-153-6 |
| 19 | 805 | 99.1 | 157 | 14 | US-10-094-153-7 |
| 20 | 805 | 99.1 | 193 | 14 | US-10-094-153-3 |
| 21 | 805 | 99.1 | 193 | 14 | US-10-094-153-4 |
| 22 | 803 | 98.9 | 157 | 12 | US-10-105-080-10 |
| 23 | 803 | 98.9 | 193 | 12 | US-10-105-080-4 |
| 24 | 801 | 98.6 | 157 | 11 | US-09-030-061-20 |
| 25 | 801 | 98.6 | 157 | 14 | US-10-100-057-20 |
| 26 | 801 | 98.6 | 157 | 15 | US-10-260-576-6 |
| 27 | 799 | 98.4 | 157 | 14 | US-10-094-153-8 |
| 28 | 799 | 98.4 | 193 | 14 | US-10-094-153-5 |
| 29 | 791 | 97.4 | 157 | 11 | US-09-030-061-21 |
| 30 | 791 | 97.4 | 157 | 11 | US-09-030-061-22 |
| 31 | 791 | 97.4 | 157 | 14 | US-10-100-057-21 |
| 32 | 791 | 97.4 | 157 | 14 | US-10-100-057-22 |
| 33 | 791 | 97.4 | 157 | 15 | US-10-260-576-7 |
| 34 | 791 | 97.4 | 157 | 15 | US-10-260-576-8 |
| 35 | 782 | 96.3 | 157 | 11 | US-09-030-061-25 |
| 36 | 782 | 96.3 | 157 | 14 | US-10-100-057-25 |
| 37 | 782 | 96.3 | 157 | 15 | US-10-260-576-11 |
| 38 | 781 | 96.2 | 157 | 11 | US-09-030-061-23 |
| 39 | 781 | 96.2 | 157 | 14 | US-10-100-057-23 |
| 40 | 781 | 96.2 | 157 | 15 | US-10-260-576-9 |
| 41 | 772 | 95.1 | 157 | 11 | US-09-030-061-26 |
| 42 | 772 | 95.1 | 157 | 14 | US-10-100-057-26 |
| 43 | 772 | 95.1 | 157 | 15 | US-10-260-576-12 |
| 44 | 771 | 95.0 | 157 | 11 | US-09-030-061-24 |
| 45 | 771 | 95.0 | 157 | 14 | US-10-100-057-24 |

ALIGNMENTS

RESULT 1
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; PRIOR FILING DATE: 2001-02-01
; PRIOR FILING DATE: 60/179,638
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

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| Query Match | | 99.9% | Score 811; | DB 10; | Length 157; |
| Best Local Similarity | | 99.4% | Pred. No. 2.1e-81; | | |
| Matches 156; | | Conservative | 0; | Mismatches 1; | Indels 0; Gaps 0; |
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| Db | 1 | YFGKLESKLSVIRNLNDQVLPIDQGNRP | LFEDMTDSCRDNAPRTIIFIISMYKDSQPRGM | 60 | |
| Qy | 61 | AVTISVKCEKISLSCENKIISFKEMNPP | DNIKDTSKDIIFQKRSVPHDNKMQFESSY | 120 | |
| Db | 61 | AVTISVKCEKISLSCENKIISFKEMNPP | DNIKDTSKDIIFQKRSVPHDNKMQFESSY | 120 | |
| Qy | 121 | EGYFLACEKERDLPFKLILKKEDELGDRS | IMFTVQNE 157 | | |
| Db | 121 | EGYFLACEKERDLPFKLILKKEDELGDRS | IMFTVQNE 157 | | |

RESULT 2
US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6
Query Match 99.9%; Score 811; DB 11; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDKMKQFESSY 120
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Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
RESULT 3
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDewitt, Damien

; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: Active IL-18 Polypeptide
; CURRENT APPLICATION NUMBER: US/10/311,491
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3
Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
RESULT 4
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; HORWOOD, Nicole Joy
; UDAGAWA, No. US20020150555A1uyuki
; KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100,057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESY 120
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Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-094-153-2
; Sequence 2, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-153-2

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6
US-10-260-576-4
; Sequence 4, Application US/10260576
; Publication No. US20030092130A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Kozo
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
```

```

; OKAMOTO, Iwao
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/260,576
; FILING DATE: 01-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. US20030092130A1ember 29, 1996
; APPLICATION NUMBER: JP 20,906/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. US20030092130A1ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US2003013292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
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TITLE OF INVENTION: IL-18 and IL-18 Combinations
FILE REFERENCE: P51144
CURRENT APPLICATION NUMBER: US/10/297,136
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/US01/17924
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/208,869
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-297-136-1

Query Match 99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISTLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8

US-09-798-075-1
Sequence 1, Application US/09798075
Patent No. US2001004418A1
GENERAL INFORMATION:
APPLICANT: Levy, Shoshana
APPLICANT: Dekryuff, Rosemarie
APPLICANT: Umetsu, Dale
APPLICANT: Maeker, Holden
TITLE OF INVENTION: Treatment of Allergies
FILE REFERENCE: STAN-179
CURRENT APPLICATION NUMBER: US/09/798,075
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/188,311
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-075-1

Query Match 99.9%; Score 811; DB 9; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 120
DB 97 AVTISVKCEKISTLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 9

US-09-770-528-8
Sequence 8, Application US/09770528
Patent No. US2002016432A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Bazan, Theodore R.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match 99.9%; Score 811; DB 10; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 120
DB 97 AVTISVKCEKISTLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKKMFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 10

US-10-311-491-1

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; Sequence 1, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-1

Query Match          99.9%; Score 811; DB 12; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 156

Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 11
US-10-311-491-10
; Sequence 10, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-10

Query Match          99.9%; Score 811; DB 12; Length 233;
Best Local Similarity 99.4%; Pred. No. 3.6e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db      77 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 136

Qy      61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120
Db      137 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 196

Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      197 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 233

RESULT 12
US-08-996-140-1
; Sequence 1, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimpei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-140-1
```

Query Match 99.8%; Score 810; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13
US-09-924-099-21
; Sequence 21, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 21
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (73)
; OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.

US-09-924-099-21

Query Match 99.8%; Score 810; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14
US-10-349-023-26
; Sequence 26, Application US/10349023
; Publication No. US20030133919A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; OKURA, Takanori
; KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,023
FILING DATE: 23-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/556,972
FILING DATE: 24-Apr-2000
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-349-023-26

Query Match 99.8%; Score 810; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKDTKSDIIFFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15
US-10-327-069-1
; Sequence 1, Application US/10327069
; Publication No. US20030129184A1
; GENERAL INFORMATION:
; APPLICANT: KASUYUKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; KENYUJO
; KUNIKATA, Toshio
; TANIGUCHI, Mutsuko
; KOHNO, Keizo
; KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE

WHICH INDUCES INTERFERON- PRODUCTION

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/327,069
FILING DATE: 24-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE: No. US20030129184A1ember 15, 1995
APPLICATION NUMBER: JP 58,240/95
FILING DATE: February 23, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-327-069-1

Query Match 99.8%; Score 810; DB 16; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

Search completed: December 12, 2003, 17:51:31
Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:50:55 ; Search time 20 Seconds
(without alignments)
754.924 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLDQVL.....LKKEDELGDRSIMFTVQNE 157
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-----------------------|
| 1 | 515 | 63.4 | 192 | S60226 | cytokine IGIF - mouse |
| 2 | 85 | 10.5 | 381 | T40341 | hypothetical prote |
| 3 | 82 | 10.1 | 263 | T39487 | hypothetical prote |
| 4 | 81.5 | 10.0 | 270 | S10532 | interleukin-1 alph |
| 5 | 80.5 | 9.9 | 866 | C71509 | probable DNA polym |
| 6 | 79 | 9.7 | 452 | D64583 | hypothetical prote |
| 7 | 78.5 | 9.7 | 204 | T44357 | hypothetical prote |
| 8 | 78 | 9.6 | 473 | T32038 | hypothetical prote |
| 9 | 77.5 | 9.5 | 1251 | A36677 | neuronal cell cycl |
| 10 | 77 | 9.5 | 364 | A81261 | probable periplasm |
| 11 | 76 | 9.4 | 632 | T00679 | hypothetical prote |
| 12 | 76 | 9.4 | 747 | E84698 | hypothetical prote |
| 13 | 75.5 | 9.3 | 192 | S15661 | (2'-5')oligo(A) sy |
| 14 | 75.5 | 9.3 | 270 | I46620 | interleukin-1 alph |
| 15 | 75.5 | 9.3 | 1036 | H64245 | hypothetical prote |
| 16 | 75.5 | 9.3 | 1663 | 1 C3MS | complement C3 prec |
| 17 | 75 | 9.2 | 1064 | 1 S7450 | protein-tyrosine k |
| 18 | 75 | 9.2 | 2470 | I50726 | cation-independent |
| 19 | 74.5 | 9.2 | 334 | T04198 | hypothetical prote |
| 20 | 74.5 | 9.2 | 389 | B89277 | TRK potassium upta |
| 21 | 74.5 | 9.2 | 467 | 2 A48713 | serine/threonine-s |
| 22 | 74.5 | 9.2 | 1228 | 2 A57384 | multimerin, endoth |
| 23 | 74.5 | 9.2 | 1510 | 2 T16927 | hypothetical prote |
| 24 | 74 | 9.1 | 245 | B90488 | hypothetical prote |
| 25 | 74 | 9.1 | 361 | E96904 | minD family ATPase |
| 26 | 74 | 9.1 | 376 | T24925 | hypothetical prote |
| 27 | 74 | 9.1 | 467 | 2 I49609 | proto-oncogene pro |
| 28 | 74 | 9.1 | 467 | 2 A47388 | serine/threonine p |
| 29 | 74 | 9.1 | 680 | 2 A28121 | major merozoite su |

virb4 protein prec
major merozoite su
probable small sub
probable small sub
seryl-cRNA synthet
hypothetical prote
interleukin-1 alph
protein P27J15.10
polynucleotide ade
hypothetical prote
p101 protein precu
probable membrane
EN2 protein - Ara
DNA helicase II BR
hypothetical prote
protein BRG1 - hum

ALIGNMENTS

RESULT 1

S60226

Cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Teutsui, H.; Komatsu, T.; Yutendo, M.; Hakura, A.; Tanimoto, T.; Torigoe,

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009; PMID:7477296

A:Accession: S60226

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;

Best Local Similarity 64.9%; Pred. No. 2.7e-4;

Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy 2 FGKLESKLSVIRNLDQVLFDIQGNRPLFEDMTDSCRDNAPRTIFITSMYKDSOPRGMA 61

Db 37 FGRHCTTAVIRNLDQVLFDVK-RQVFEDMTDIDQASSEPQTRLIIMYKDSVRLA 95

Qy 62 VTISVKCEKISXLSCEKNKIISFKEMNPPDNIKOTKSDIIFQSRVPGHDNNKQFESSSYE 121

Db 96 VTLGVKDSKMSLTSCKNKIISFEMDPPENIDDIQSDLIFFQKRVPGH-NKMBFESSLYE 154

Qy 122 GYFLACEKERDLPFKLILKKEDELGDRSIMFTVQN 155

Db 155 GHFLACQKEDDAFKLILKKEDELGDRSIMFTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40341

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z21922

A:Accession: T40341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL022070; PIDN:CAA17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:

A:Gene: SPDB:SPBC3B9.02c

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N:Alternate names: hematopoietin-1; IL-1 alpha
C:Species: Sus scrofa domestica (domestic pig)
C:date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
C:Accession: S10532
R:Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.
Nucleic Acids Res. 18, 4282, 1990
A:title: Porcine IL-1 alpha cDNA nucleotide sequence.
A:Reference number: S10532; MUID:90332454; PMID:2377484
A:Accession: S10532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <MAL>
A:Cross-references: EMBL:X52731; NID:g1987; PIDN:CRAA36945.1; PID:g1988

hypothetical protein HP0508 - *Helicobacter pylori* (strain 26695)
 C:Species: *Helicobacter pylori*
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: D64583
 R:Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

```

Db      758 QDKQALELDLQAKERDLAKVQITSTS--SEKSYBFKIMEE 797
      : : : : : : : : : : : : : : : : : : : : : :
      RESULT 10
      A81261
      probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11637)
      C;Species: Campylobacter jejuni
      C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
      C;Accession: A81261
      R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketlev, J.M.; Churcher, C.; Basham, D.;

```

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: A81261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: CJ1643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 8.9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRLNQVLFIDQGNRPLFEDMTDSCRD-NAPRTIFIISMYK----DSQPR----- 58
Db 211 LRKLNKILFADRGSTLYFQVLRDN--MDLNISTEVEFAKDLKFNLPDSKPKITNFTS 268
QY 59 --GMATISVCKEKI-----SXLSCKENII-SPEKNPPDNI----- 92
Db 269 NLGLTYNASLVWTKIDPKSKVSNAGFMVGDKILRVNNIILNPKEL---QNILSAGNDFS 325
QY 93 -----KDTKSDIIFQFVSFGH-----DNKMQF 115
Db 326 ILIERKSTKLPLSNFNFELGGNANSNGDGKQF 358

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00679; A84873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: T00679
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;
Best Local Similarity 25.8%; Pred. No. 21;
Matches 34; Conservative 29; Mismatches 40; Indels 30; Gaps 9;

QY 28 PLFEDMTSD-CRDNAPRTIFIISMYKDSQPRGMATISVCKE-----ISXLSCKENK 79
Db 368 PLSDRASDCLNWSGRSLSPMDIYKETR---ISSLSPLNLPFRFRFHLSCDGE 424
QY 80 IISFK-----ENPPNIIKDTSDIIFQFVSFGH-----ESSYEGYF-LACK 129
Db 425 ASAFDTSPTCELDPSHLKGDKSSPL-----SVDTLGSENVITQPSNSSFDFNLGSLSCQ 480

QY 130 ERDLFKLILKKED 142
Db 481 AE-----IQKKHD 488

RESULT 12

E84698

hypothetical protein At2g29620 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: E84698

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84698

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-747 <STO>

A:Cross-references: GB:AE002093; NID:g3582336; PIDN:AAC35233.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g29620

A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 747;

Best Local Similarity 24.7%; Pred. No. 26;

Matches 36; Conservative 29; Mismatches 59; Indels 22; Gaps 7;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGMAT 63

Db 102 KUKHQOSVVRNARRKV-----EEVGKDWDSQASEDERGKVLTLTGEVLPE---T 150

QY 64 ISVCKEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQF---SVPGHDKMQF---SS 118

Db 151 ITPDMKFKP---RERTLLVAEENVFSDVLDNRDLVELERLISVDG-DDESEVECSSS 205

QY 119 SVYEGYFLACEKRDPLFKILK-KEDE 143

Db 206 SSEGEKEEEREDVSKVVAVWTEDD 231

RESULT 13

S15661

(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999

C:Accession: S15661; S19108

R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.

Nucleic Acids Res. 19, 1917-1924, 1991

A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked ge

A:Reference number: S15660; MUID:91232962; PMID:1709495

A:Accession: S15661

A:Molecule type: mRNA

A:Residues: 1-192 <RUT>

A:Cross-references: EMBL:X55982

submitted to the EMBL Data Library, September 1990

A:Reference number: S19108

A:Accession: S19108

A:Molecule type: mRNA

A:Residues: 1-175, 'L', 177-192 <WIL>

A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715

C:Superfamily: oligo(A) synthetase

C:Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;

Best Local Similarity 23.2%; Pred. No. 5.8;

Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKD 54

Db 11 GRSDADLVVFLNLTSPFQDLNOQGLVLIKEIKQLCEVQHERRC----- 54
Qy 55 SQPRGMVAVTSVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDII----- 100
Db 55 -----GVKFEVSLRSPNRSALSK-LSAPDLLKEVDFVLPAYDLLDHLNLUKK 103
Qy 101 ----FFOR---SVP-GHDNKNQFESSYEGYFLACE--KERDLFKLI-----LKKEDBLG 145
Db 104 PNQOFYANLISGVPAKGEGSLSCFMGLQKYFLNCRPTKRLRLRLVTHWYQLCKE-KLG 162
Qy 146 D 146
Db 163 D 163

RESULT 14

I46620

interleukin-1 alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000

C:Accession: I46620

R:Maliszewski, C.

Nucleic Acids Res. 14, 4282, 1990

A:Title: Nucleotide sequence of porcine interleukin-1 alpha.

A:Reference number: I46620

A:Accession: I46620

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-270 <MAL>

A:Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623

C:Superfamily: interleukin-1

C:Keywords: lipoprotein; myristylation

F:1-112/Domain: propeptide #status predicted <PRO>

F:113-270/Product: interleukin-1 alpha #status predicted <ILI>

F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;
Best Local Similarity 22.0%; Pred. No. 8.7;
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

Qy 8 KLSVIRNLNDQVLFDQGNRPLFEDMTD-----SCDRDNAPRTI-FIISMYKDSQPRGMNAV 62
Db 123 KYNFMRVINHQCILNDARNQSIIRDPSQQLMAAVLNNLDEAVKFDMAAYTSNDDSQLPV 182
Qy 63 TISVKCEKISXLSCE--KIISFKEM-NPPDNIKDTKSDIIFQORSVPGHDNKNQFESS 119
Db 183 TLRIS-ETRLFVSAQNEDEPVLKELPPTKTIKDTSLFFWEK----HGNMDYFKSAA 237
Qy 120 YEGYFLACEKER 131
Db 238 HPKLLIATRQEK 249

RESULT 15

H64245

hypothetical protein MG414 - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001

C:Accession: H64245; G64245

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346; PMID:7569993

A:Accession: H64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1036 <TIGR>

A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414

A:Experimental source: strain G-37

A:Accession: G64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 310-1036 <TIG2>
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
A:Start codon: GTG
C:Superfamily: hypothetical protein MG413

Query Match 9.3%; Score 75.5; DB 2; Length 1036;
Best Local Similarity 21.9%; Pred. No. 43;
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

Qy 14 NLNDQVLFDQGNRPLFED--MTDSCDRDNAPRTIFIISMYKDSQPRGMNAVTSVKCEK- 70
Db 845 SLNDEQLLVKLNITLSEKBLQTTKVRFLNKNKFINHLVENKNQNLVFDVDRSKL 904
Qy 71 -ISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKNQFSSSYEGYFLACEK 129
Db 905 FIKGVNNDNQVFSISY----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
Qy 130 ERDLFKLI---LKKEDLGRSIMPFTVQNE 157
Db 951 QTQLFKALSPYLKQNNLQPKRVDPDFNLKSQD 981

Search completed: December 12, 2003, 17:54:16

Job time : 21 secs

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